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Pate of Deposit: August 9, 2001



PATENT APPLICATION
Attorney Docket No.: 19904-008

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANTS: Rouquier et al.

SERIAL NUMBER: 09/747,155 EXAMINER: Not Yet Assigned

FILING DATE: December 21, 2000 ART UNIT: 1645

FOR: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

August 9, 2001

Boston, Massachusetts

BOX MISSING PARTS

Assistant Commissioner for Patents Washington, D.C. 20231

STATEMENT IN SUPPORT OF COMPUTER READABLE FORM SUBMISSION UNDER 37 C.F.R. § 1.821(f)

Sir

I hereby state that the content of the paper and computer readable form of the Sequence Listing, submitted in the above-identified application in accordance with 37 C.F.R. § 1.821(c) and 1.821(e), respectively, are the same. No new matter has been added.

Respectfully submitted,

Mathew Pavao

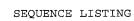
c/o MINTZ, LEVIN

One Financial Center

Boston, Massachusetts 02111

Tel: (617) 542-6000 Fax: (617) 542-2241

TRA 1553048v1







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Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser 165 170

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Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His 50

Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val

Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met 90 85

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys 105 100

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 125 120

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu 130

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser

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Thr Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Phe Ser Val Leu Arg
145
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Ile Ser Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
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Val Met Tyr Thr Val Val Thr Pro

180 185 190

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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Ser Leu His 50 55 60

Tyr Thr Val Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Leu Gly 65 70 75 80

Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val 85 90 95

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Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn 115 120 125

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145					150					155					160		
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Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Ile Ile Ile
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 Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Val
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His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
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Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val

Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys 100

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 120

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Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val 65 70 75 80	

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Met	Ser	Ser	Ser	Gly 165	Gly	Lys	Gln	Lys	Ala 170	Leu	Ser	Thr	Cys	Gly 175	Ser		
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Phe	Thr	Ser 195	Ala	Val	Thr	His	Ala 200	Ser	Gln	Lys	Ile	Ser 205	Val	Ala	Ser		
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Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu 130 135

Met Met Ile Phe Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys 155 150

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His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr 185

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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 60

Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80

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Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His Phe Cys 100 105 110

Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

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Asn Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175

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Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala

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Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val

Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg

Thr Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 170

His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190

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140

433

481

gac atg atg atg aat ttt aca agt gtg ctg ttg ggt ggg gga tgc ctc

Asp Met Met Met Asn Phe Thr Ser Val Leu Leu Gly Gly Gly Cys Leu

gct gga ata ttt tac tct tac ttt aag ata ctt tgt tgc ata tgt tca

Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Leu Cys Cys Ile Cys Ser

135

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cac His	ctc Leu	tca Ser	gtt Val 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	tgt Cys	aca Thr	ggc Gly	gta Val	ggt Gly 190	gtg Val	tac Tyr	577
ctt Leu	agt Ser	tct Ser 195	gct Ala	gca Ala	acc Thr	cat His	aac Asn 200	tca Ser	ctc Leu	tca Ser	aat Asn	gct Ala 205	gca Ala	gcc Ala	tca Ser	625
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Sei	r Tr	o Ile	e Val	. Ser 85	: Ile	. Leu	. Cys	Ser	90	Leu	Glr.	ser	: Ile	e Met 95	. Ala	
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Gli	u Lei	u Ası 11!		ı Val	l Val	His	120		а Сув	s Sei	As <u>r</u>	125	r Pho	e Ile	e Lys	\$
As	р Ме 13		t Met	Asr	ı Phe	Thr 135		. Val	L Let	ı Let	1 Gly	y Gly	y Gl	у Су	s Leu	1

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Ile Ser Pro Ala Gln Gly Met Asn Lys Ala Leu Ser Thr Cys Ala Ser
His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Val Gly Val Tyr
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 aac atc cag gca cgg atc aaa gac atc tcc tac atg ggg tgc ctc act
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 Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
                              40
 gec gtg atg gec tat gac egg ttt gtg gec ate tge eac eec etg eac
                                                                          193
 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
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 tac acg gtc atc atg aac ccc tgc ctc tgt ggc ctc ctg gtt ctg gca
                                                                          241
 Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
                      70
 65
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                                                                          289
 Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile Leu Leu Met
 aag aag ttg acc ttc tcc aca ggc act gag att ccg cat ttc ttc tgt
                                                                          337
 Lys Lys Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
                                   105
 gaa ccg gct cag gtc ctc aag gtg gcc tgc tct aac acc ctc ctc aat
Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn
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Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile
165 170 175

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Ser Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr

180

185

190

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195 200 205

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Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 60

Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80

Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile Leu Leu Met 85 90 95

Lys Lys Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Cys 100 105 110

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Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
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Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile
Ser Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
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AF127849
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                                                                       300
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                                                                       360
 tgactgttct gaacagtgtc atcaatagca tattcacata tttagatagt actatgtttg
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600 650

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tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgaccgg tttgtagcca
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totgtcacco totatatoat toagocatoa tgaaccogtg titotgtggo ticotagatt
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tgccttacaa atgacctgct tcgaggatgt gggaattcct aatttcctct gtgacccttc
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tcaactgccc catctcacat gttgtgacat cttcaccaat cacataatca tgtatttccc
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                                                                      480
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ttgtttgctg atattatgga acaggetteg gagggtaeet eagtteagat gtgttatett
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 aat ata ctg aca cag aac aaa ttc ata aca tat gca ggc tgt ctc ggt
                                                                       97
 Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly Cys Leu Gly
 cag att ttt ttt ttc act tca ttt gga tgc ctg gac aat tta ctc ttg
                                                                       145
 Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn Leu Leu
 act gtg atg gcc tat gac cgc ttc gtg gcc atc tgt cac ccc ctg cac
                                                                       193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
                                             60
 tat acg gtc atc atg aac ccc cgg ctc tgt gga ctg ctg gtt ctg ggg
                                                                       241
 Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Gly
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55

60

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75
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Thr Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Val Phe Ser Ile Leu Arg
                                        155
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Ile Ser Ser Ala Gly Arg Lys His Lys Ala Phe Ser Thr Cys Gly Ser
                165
                                     170
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Phe Gly Val Tyr
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Gln Met Cys Phe Val Leu Gly Ser Ala Thr Leu Glu Asn Phe Leu Leu

35 40 45

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atg Met	gca Ala	tca Ser	gca Ala	agt Ser 165	gga Gly	aag Lys	tat Tyr	aaa Lys	gct Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	ggc Gly 175	tct Ser	529	
cac His	ctc Leu	tcg Ser	gtt Val 180	Val	tcc Ser	ttg Leu	ctc Leu	tac Tyr 185	Gly	aca Thr	ggt Gly	ttg Leu	999 Gly 190	gtg Val	tac Tyr	577	
atc Ile	agt Ser	tct Ser 195	Ala	ttt Phe	atg Met	cac His	tct Ser 200	Pro	agg Arg	acg Thr	atg Met	gca Ala 205	Val	gct Ala	tca Ser	625	
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Gln Met Cys Phe Val Leu Gly Ser Ala Thr Leu Glu Asn Phe Leu Leu

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg

Tyr Ala Val Ile Met Asn Leu Arg Leu Cys Gly Phe Leu Ile Leu Leu 70

Ser Leu Ser Ile Ser Ile Met Asp Thr Leu Leu His Asp Leu Met Val

Leu Arg Leu Ser Phe Cys Thr His Leu Glu Ile Pro Leu Phe Phe Cys 105

Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr Leu Ile Asn

Asn Leu Leu Ile Tyr Phe Ala Ala Gly Val Leu Gly Gly Val Pro Leu 135

Ser Gly Ile Ile Phe Ser Tyr Thr Gln Ile Ala Ser Ser Val Leu Arg 150

Met Ala Ser Ala Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser

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acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc ctg cac Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60	193
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atg tcc tcc act tca gca aag aat aaa gca ttt tcc acc tgt ggg tct Met Ser Ser Thr Ser Ala Lys Asn Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175	529
cac ctc tgt gtg gtc tct ttg ttc tat gga act gca ctt ggg gtc tac His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Gly Val Tyr 180 185 190	577
ctc agc tct gct gtg acc cct tct tcc cag agc agc gcc att gcc tca Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ala Ile Ala Ser 195 200 205	625
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Met Val Ile Met Asn Pro Arg Phe Cys Ala Leu Leu Val Leu Met 65 70 75 80

Ser Trp Phe Ile Met Ser Leu Val Ala Leu Val His Val Leu Leu Ile 85 90 95

Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Ser Cys 100 105 110

Glu Val Ala Gln Ile Leu Lys Val Ala Arg Ser Asp Thr Phe Phe Asn 115 120 125

Asn Ile Cys Leu Tyr Leu Ser Ala Val Leu Leu Gly Val Phe Pro Val 130 135 140

Met Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg 145 150 155 160

Met Ser Ser Thr Ser Ala Lys Asn Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Gly Val Tyr \$180\$

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Val Met Tyr Thr Val Val Thr Pro 210 215

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gtg cag aca tgg agc aaa gtc ata tct tac aca ggc tgc atc acc cag
                                                                       97
Val Gln Thr Trp Ser Lys Val Ile Ser Tyr Thr Gly Cys Ile Thr Gln
            2.0
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                                                                      145
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Met Asp Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu Thr
                             40
                                                                      193
gtg atg gcc tat gac egg ttt gtg gcc atc tgt cac eec etg egc tat
Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr
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                         55
                                             60
gea gtc atc atg aac ccc agg ctc tgt gta ttt ctt gtt ctg gtg tcc
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cgg cta acc tt Arg Leu Thr Ph 10	e Cys Thr As	ac ttg gaa sp Leu Glu 105	atc ccc cac Ile Pro His	ttt ttc tgt Phe Phe Cys 110	gaa 337 Glu
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ggg atc ctt ta Gly Ile Leu Ty 145	c tot tac to or Ser Tyr S 150	ct aag ata er Lys Ile	gtt tcc tcc Val Ser Ser 155	gta cgt gca Val Arg Ala	atc 481 Ile 160
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ctc ttg gtc gt Leu Leu Val Va 18	al Ser Leu P	tt tat tgt he Tyr Cys 185	Thr Cys Le	a ggg gtg tac ı Gly Val Tyr 190	ttg 577 Leu
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Met Asp Phe P 35	he Leu Leu l	Phe Val Gly 40	y Leu Asp As	n Phe Leu Le 45	ı Thr
Val Met Ala T 50		Phe Val Ala 55	a Ile Cys Hi 60		g Tyr

Ala Val Ile Met Asn Pro Arg Leu Cys Val Phe Leu Val Leu Val Ser Trp Ile Leu Ser Val Leu Asn Ser Leu Ser Gln Ser Leu Met Val Leu 90 Arg Leu Thr Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys Glu 100 105 Leu Asn Gln Ile Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Val Met Leu Leu Gly Gly Cys Leu Thr 135 Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala Ile Ser Ser Ala Gln Gly Lys Cys Lys Ala Phe Ser Thr Cys Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Cys Thr Cys Leu Gly Val Tyr Leu 180 Ser Ser Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser Val Met 200 195 Tyr Thr Val Val Thr Pro 210 <210> 67 <211> 644 <212> DNA <213> Eulemur rubriventer <220> <221> misc_feature <222> (1)..(644) nk

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ccca	ctct	ga c	ccct	ccat	c aa	taat	gtca	tat	tata	cat	tgtg	acgg	tg t	catg	ggctt	42	20
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ctca	acag	ca g	gggg	gaag	t at	aaag	tgtt	ttc	ctcc	tgt	gagt	ctca	cc t	ctcg	gttgt	54	10
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cag Gln	atg Met	tac Tyr 35	ttc Phe	ttc Phe	atg Met	gcc Ala	ctt Leu 40	gca Ala	aac Asn	act Thr	gac Asp	agc Ser 45	tac Tyr	cta Leu	ctg Leu	1	45
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gat Asp	acc Thr	cag Gln 115	cct Pro	gtg Val	cta Leu	aag Lys	ctt Leu 120	tcc Ser	tgc Cys	tct Ser	gac Asp	aca Thr 125	tcc Ser	tcc Ser	agc Ser	3	885
cag Gln	att Ile 130	gtg Val	gtc Val	atg Met	acc Thr	gag Glu 135	acc Thr	ctg Leu	gct Ala	gtc Val	atc Ile 140	gtg Val	acc Thr	ccc Pro	ttc Phe	4	133
ctg Leu 145	tgc Cys	atc Ile	atc Ile	ttc Phe	tcc Ser 150	Tyr	ctg Leu	aga Arg	atc Ile	atc Ile 155	Ile	act Thr	gtg Val	ctc Leu	gca Ala 160	4	181

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Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 115 120 125	
Gln Ile Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 130 135 140	
Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Ala	

Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser 165 $$ 170 $$ 175 $$

His Leu Thr	Val Val 180	Val Leu	Phe	Tyr 185	Gly	Ser	Val	Ile	Tyr 190	Val	Tyr	
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cag atg gac Gln Met Asp 35	ttc ttt Phe Phe	gta cto Val Lei	ttt Phe 40	gta Val	gly aaa	ctg Leu	gac Asp	agc Ser 45	ttc Phe	ctc Leu	ctt Leu	145
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tac gcg gtc Tyr Ala Val 65												241
tct tgg atc	atg agt											
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Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala 155 145 150

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170

His Leu Ala Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr 190

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 Gln Met Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu
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 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
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 Tyr Thr Val Ile Met Ser Pro Arg Phe Cys Ala Leu Leu Val Leu Ile
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Tyr Thr Val Ile Met Ser Pro Arg Phe Cys Ala Leu Leu Val Leu Ile

Ser Trp Phe Ile Met Thr Leu Val Ala Leu Val His Val Leu Leu Ile

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Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys 100 105 110

Glu Leu Asn Gln Val Ile His Leu Thr Cys Ser Asp Thr Phe Leu Asn 115 120 125

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Ile Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile His Ala 145 150 155 160 Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175

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433

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Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe

130 135 140

tca Ser 145	gga Gly	atc Ile	ctt Leu	ttc Phe	tcc Ser 150	tac Tyr	acc Thr	caa Gln	att Ile	gtc Val 155	tcc Ser	tcc Ser	atc Ile	ctg Leu	aga Arg 160	481	
atc Ile	tca Ser	tcc Ser	Thr	gat Asp 165	gly aaa	aaa Lys	cac His	aaa Lys	gcc Ala 170	ttt Phe	tct Ser	aac Asn	tgc Cys	gga Gly 175	tct Ser	529	
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His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
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Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Ile Val

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 100 105 110

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tac Tyr 65	acc Thr	aca Thr	gcc Ala	atg Met	agc Ser 70	cct Pro	aag Lys	ctc Leu	tgt Cys	atc Ile 75	tta Leu	ctc Leu	ctt Leu	tcc Ser	ttg Leu 80	241
tgt Cys	tgg Trp	gtc Val	tta Leu	tct Ser 85	gtg Val	ctc Leu	tat Tyr	ggc Gly	ctc Leu 90	ata Ile	cac His	acc Thr	ttc Phe	ctc Leu 95	atg Met	289
acc Thr	acg Thr	gtg Val	acc Thr 100	ttc Phe	tgt Cys	ggg ggg	tca Ser	cga Arg 105	aaa Lys	atc Ile	cac His	tac Tyr	atc Ile 110	ttc Phe	tgt Cys	337
gag Glu	atg Met	tat Tyr 115	Val	ttg Leu	ctg Leu	agg Arg	ctg Leu 120	A⊥a	tgt Cys	tcc Ser	gac Asp	act Thr 125	cag Gln	att Ile	aat Asn	385
cac His	aca Thr 130	Val	ctg Leu	att Ile	gcc Ala	aca Thr 135	ggc	tgc Cys	ttt Phe	atc Ile	ttc Phe 140	ctc Leu	att Ile	ccc Pro	ttt Phe	433
gga Gly 145	Phe	atg Met	atc Ile	att Ile	tcc Ser 150	Tyr	gtg Val	ttg Leu	att Ile	gtc Val 155	aga Arg	gcc Ala	atc Ile	ctc Leu	aga Arg 160	481
ata Ile	ccc Pro	tca Ser	gtc Val	tct Ser 165	. Ta	aaa Lys	tac Tyr	aaa Lys	gcc Ala 170	Phe	tcc Ser	act Thr	tgt Cys	gcc Ala 175	Ser	529
cat His	tto Lev	ggt Gly	gta Val	Val	tcc Ser	ctc Leu	tto Phe	tate Tyr	: GIY	aca Thr	ctt Leu	cgt Arg	ato Met	. var	tac Tyr	577
ctg	, aag	g cco	c ctc	c cat	acc	tac	: tct	gtg	g aag 73		tca	gta	gc.	aca	gtg	625

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Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Ser Leu
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Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr Phe Leu Met
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Thr Thr Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys
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 Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asp Thr Gln Ile Asn
                             120
 His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Phe
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 Gly Phe Met Ile Ile Ser Tyr Val Leu Ile Val Arg Ala Ile Leu Arg
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 Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
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Met Tyr Ala Val Val Thr Pro 210 215

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cag Gln	gtc Val	tat Tyr 35	ttc Phe	tcc Ser	atg Met	ttt Phe	ttt Phe 40	cct Pro	att Ile	ctg Leu	gac Asp	acg Thr 45	cta Leu	ctc Leu	ctg Leu	145
acc Thr	gtg Val 50	atg Met	gct Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	gtc Val	tgc Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tat Tyr 65	gta Val	acc Thr	atc Ile	atg Met	aac Asn 70	ccc Pro	cgc Arg	ctc Leu	tgc Cys	ggc Gly 75	ctc Leu	ctg Leu	gtt Val	ttt Phe	gtc Val 80	241
acg Thr	tgg Trp	ctc Leu	att Ile	ggt Gly 85	gtc Val	atg Met	aca Thr	ccc Pro	ctc Leu 90	ctc Leu	cat His	att Ile	tct Ser	ctg Leu 95	ttg Leu	289
acg Thr	cat His	cta Leu	acc Thr 100	ttc Phe	tgt Cys	aaa Lys	gat Asp	ttt Phe 105	gaa Glu	att Ile	cca Pro	cat His	ttt Phe 110	ttc Phe	tgc Cys	337
gaa Glu	ctg Leu	aca Thr 115	cac His	atc Ile	ctc Leu	cag Gln	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	acc Thr 125	ttc Phe	ctg Leu	aac Asn	385
agc Ser	acg Thr 130	ttg Leu	ata Ile	tat Tyr	gtt Val	atg Met 135	aca Thr	ggt Gly	gtg Val	ctg Leu	ggc Gly 140	gtt Val	ttt Phe	ccc Pro	ctc Leu	433
ctt Leu 145	Gly aaa	atc Ile	att Ile	ttc Phe	tct Ser 150	tat Tyr	tca Ser	cga Arg	atc Ile	gct Ala 155	tca Ser	tcc Ser	ata Ile	agg Arg	aag Lys 160	481

atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct 529

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cac His	ctc Leu	tcc Ser	atc Ile 180	gtt Val	tct Ser	tta Leu	ttt Phe	tat Tyr 185	gly ggg	aca Thr	ggc Gly	att Ile	999 Gly 190	gtc Val	cat His	577
ttc Phe	act Thr	tct Ser 195	gcg Ala	gtg Val	act Thr	cat His	tct Ser 200	tcc Ser	cag Gln	aac Asn	atc Ile	tcc Ser 205	gtg Val	gcc Ala	tcg Ser	625
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Gln	Val	Tyr 35	Phe	Ser	Met	Phe	Phe 40	Pro	Ile	Leu	Asp	Thr 45	Leu	Leu	Leu	
Thr	Val 50	Met	Ala	Tyr	Asp	Arg 55	Phe	Val	Ala	Val	Cys 60	His	Pro	Leu	His	
Tyr 65	Val	Thr	Ile	Met	Asn 70	Pro	Arg	Leu	Cys	Gly 75	Leu	Leu	Val	Phe	Val 80	
Thr	Trp	Leu	Ile	Gly 85	Val	Met	Thr	Pro	Leu 90	Leu	His	Ile	Ser	Leu 95	Leu	
Thr	His	Leu	Thr 100	Phe	Cys	Lys	Asp	Phe 105		Ile	Pro	His	Phe 110		Cys	
Glu	Leu	Thr 115		Ile	Leu	Gln	Leu 120		. Cys	Ser	Asp	Thr 125		Leu	Asn	
Ser	Thr 130		Ile	Tyr	Val	Met 135		Gly	Val	Leu	Gly 140		Phe	Pro	Leu	
Leu 145		Ile	· Ile	Phe	Ser 150	Tyr	Ser	Arg	, Ile	Ala 155		Ser	· Ile	Arg	Lys 160	

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Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
                165
His Leu Ser Ile Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
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Val Met Tyr Thr Val Val Thr Pro
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                                                                      180
tgctggaatg gatactttcc tactggccat gatggcctat gaccggtttg tggccatctg
ccacccctg cactacacgg tcatcatgaa cccctgcctc tgtggcatcc tggttctggc
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atcttgattc atcattttat gggtctccct agttcatatt ctactgatga agagtttgat
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ctccataggc actgagattc cgcatttctt ctgtgaactg gctcaggtcc tcaaggtgcc
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cgctctgata ctctcctcgt taacattgtc ttgtatgtgg ccacagcact gctgggtgtg
                                                                      420
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                                                                      480
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Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Al	a Gly Cys Ile Ser
20 25	30
cag atg tat ttt ttc atg gtt ttt gga ggc ata ga	tc aca ttt ctc ctc 145
Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile As	p Thr Phe Leu Leu
35 40	45
acc gtg atg gcc tat gac cgg tat gtg gcc atc tg Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cy 50 55	rs His Pro Leu Tyr
tac cct gtc att atg aac ccc cgc ctc tgt ggc ct	eg ctg gtt ctt gtg 241
Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Le	eu Leu Val Leu Val
65 70 75	80
tcc tgg ttc ctc agc ttg tca tac tcc ctg atc ca	ag agt ctg ttg atg 289
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gl	In Ser Leu Leu Met
85 90	95
ctg cag ttg tcc ttt tgc acc agt tgg gtc att ca	ag cac ttt tac tgc 337
Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile G	ln His Phe Tyr Cys
100 105	110
gag ctt gct cag gcc ctc acg ctt gcc tgc tca ga	ac aca cac atc aat 385
Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Aa	sp Thr His Ile Asn
115 120	125
tac atc ctg ctc tac gtg gtg acc ggc ctt ctg gg	gt ttt gtg ccc ttc 433
Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu G	ly Phe Val Pro Phe
130 135	40
tca gga atc ctt ttc tcc tac acc caa att gtc t	cc tcc atc ctg aga 481
Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val S	er Ser Ile Leu Arg
145 150 155	160
atc tca tcc aca gat ggg aaa cac aaa gcc ttt t	ct acc tgc gga tct 529
Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe S	er Thr Cys Gly Ser
165 170	175
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His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr G	ly Leu Gly Val Tyr
180 185	190
ctt agt tcc aat gca tcg tcc tct tcc tgg cgg g	gc atg gtg gcc tcg 625
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Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val 75

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met

Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys

Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn 115 120

Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe

Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg

Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser 165

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														ctc Leu		145
acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tac Tyr 65	acg Thr	gtc Val	atc Ile	atg Met	aac Asn 70	cct Pro	cag Gln	ttc Phe	tgt Cys	gga Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gtg Val 80	241
														atg Met 95		289
														ttc Phe		337
gaa Glu	att Ile	cat His 115	cag Gln	ata Ile	att Ile	caa Gln	ttt Phe 120	gcc Ala	tgt Cys	tct Ser	gac Asp	acc Thr 125	ttt Phe	ctt Leu	aat Asn	385
														ccc Pro		433
gct Ala 145	Gly aaa	atc Ile	ctg Leu	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gct Ala 155	tcc Ser	tct Ser	ata Ile	cgt Arg	gca Ala 160	481
														gca Ala 175		529
cac His	ctc Leu	tca Ser	gtt Val 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	tgt Cys	aca Thr	ggc Gly	cta Leu	999 Gly 190	gtg Val	tac Tyr	577
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

Tyr Thr Val Ile Met Asn Pro Gln Phe Cys Gly Leu Leu Val Leu Val

Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Val

Tyr Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro Gln Phe Phe Cys

Glu Ile His Gln Ile Ile Gln Phe Ala Cys Ser Asp Thr Phe Leu Asn

Asn Leu Val Met Tyr Leu Ser Thr Val Leu Leu Gly Gly Pro Leu 130 135

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala 145 150

Ile Ser Ser Ala Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170 165

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aac atc cag gag cag agt ggt acc atc agc tat gca ggc tgc att gcc
                                                                         97
Asn Ile Gln Glu Gln Ser Gly Thr Ile Ser Tyr Ala Gly Cys Ile Ala
cag atg tat ttt ttc atg gtt ttt gga ggc atg gac aca ttt ctc ctc Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr Phe Leu Leu
                                                                        145
act gtg atg gcc tat gac cgg tat gtg gct atc tgt cac ccc ctg tcc
                                                                         193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Ser
                                                                         241
tac cct gtc att gta aac ccc cgc ctc tgc ggc ctg ttg gtt ctt gtg
Tyr Pro Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
65
tcc tgg ttc ctc agc ttg tca tac tcc ctg atc cag agt ctg ttg atg
                                                                         289
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
                 85
                                      90
ctg cgg cta tcc ttc tgc acc agt tgg gtc att cag cac ttt tac tgt
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Leu Arg Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
                                 105
gag ctt gct cag gtt ctc acg ctt gcc tgc tca gac aca cat gtc aat
                                                                        385
Glu Leu Ala Gln Val Leu Thr Leu Ala Cys Ser Asp Thr His Val Asn
                             120
                                                  125
tac atc ctg ctc tac atg gtg acc ggc ctt ctg ggc tgt gtt ccc ttc
                                                                         433
Tyr Ile Leu Leu Tyr Met Val Thr Gly Leu Leu Gly Cys Val Pro Phe
tca ggg atc ctt ttc tcc tac atc caa att gtc tcc tcc atc ctg aga
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Ser Gly Ile Leu Phe Ser Tyr Ile Gln Ile Val Ser Ser Ile Leu Arg
145
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                                          155
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Ile Pro Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser
                                                                         577
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His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
            180
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Thr Val Met Ala Tyr Asp Arg Ty 50 55	vr Val Ala Ile Cys 60	His Pro Leu Ser
Tyr Pro Val Ile Val Asn Pro Ar 65 70	g Leu Cys Gly Leu 75	Leu Val Leu Val 80
Ser Trp Phe Leu Ser Leu Ser Ty 85	yr Ser Leu Ile Gln 90	Ser Leu Leu Met 95
Leu Arg Leu Ser Phe Cys Thr Se	er Trp Val Ile Gln 105	His Phe Tyr Cys 110
Glu Leu Ala Gln Val Leu Thr Le 115 12		Thr His Val Asn 125
Tyr Ile Leu Leu Tyr Met Val Th	nr Gly Leu Leu Gly 140	Cys Val Pro Phe
Ser Gly Ile Leu Phe Ser Tyr Il 145 150	e Gln Ile Val Ser 155	Ser Ile Leu Arg 160
Ile Pro Ser Thr Asp Gly Lys Hi 165	s Lys Ala Phe Ser 170	Thr Cys Gly Ser 175
His Leu Ser Val Val Ser Leu Ph 180	ne Tyr Gly Thr Gly 185	Leu Gly Val Tyr 190

Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Trp Gly Met Val Ala Ser 195 200 205

Ala Met Tyr Thr Val Val Thr Pro 210 215

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caa atg tac ttc to Gln Met Tyr Phe Pl 35	c atg gcc ttt ne Met Ala Phe 40	ggg aac act Gly Asn Thr	gac agc tac ctg Asp Ser Tyr Leu 45	ctg 145 Leu
gcc tct atg gcc at Ala Ser Met Ala II 50	ic gac cgg ctg le Asp Arg Leu 55	g gtg gcc atc Val Ala Ile	tgc aac ccc tta Cys Asn Pro Leu 60	cac 193 His
tat gat gtg gct at Tyr Asp Val Ala Me 65	ng aac ccc cgg et Asn Pro Arg 70	cat tgc cta His Cys Leu 75	ctc atg cta ttg Leu Met Leu Leu	ggt 241 Gly 80
tot tgc agc atc to Ser Cys Ser Ile Se 89	er His Leu His	tcc ctg ttc Ser Leu Phe 90	cgg gtg cta ctt Arg Val Leu Leu 95	atg 289 Met
tot cac ctg tot to Ser His Leu Ser Ph 100	cc tgt gcc tcc ne Cys Ala Ser	cac gtc att His Val Ile 105	aag cac ttt ttc Lys His Phe Phe 110	tgt 337 Cys
gac acc cag cct gt Asp Thr Gln Pro Va 115	g cta aag ctg al Leu Lys Leu 120	Ser Cys Ser	gac acg tcc tcc Asp Thr Ser Ser 125	agc 385 Ser
cag atg gtg gtc at Gln Met Val Val Me 130				
ctg tgt atc atc to Leu Cys Ile Ile Ph 145				

atc ccc Ile Pro	ttt g Phe A	gca gct Ala Ala 165	Gly	aag Lys	tgg Trp	agg Arg	gcc Ala 170	ttc Phe	tct Ser	acc Thr	tgt Cys	ggc Gly 175	tcc Ser	529
cac ctc His Leu	Thr V	gta gta Val Val 180	gcc Ala	ctt Leu	ttc Phe	tac Tyr 185	Gly aaa	agt Ser	ata Ile	tat Tyr	tat Tyr 190	gtc Val	tat Tyr	577
ttt agg Phe Arg	ccc c Pro I 195	ctg tco Leu Ser	atg Met	tac Tyr	tca Ser 200	gtg Val	gtg Val	aag Lys	gac Asp	cga Arg 205	gta Val	gcc Ala	aca Thr	625
gtt atg Val Met 210														649
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Gln Met	Tyr P 35	Phe Phe	Met	Ala	Phe 40	Gly	Asn	Thr	Asp	Ser 45	Туг	Leu	Leu	
Ala Ser 50	Met A	Ala Ile	Asp	Arg 55	Leu	Val	Ala	Ile	Cys	Asn	Pro	Leu	His	
Tyr Asp 65	Val A	Ala Met	Asn 70	Pro	Arg	His	Cys	Leu 75	Leu	Met	Leu	Leu	Gly 80	
Ser Cys	Ser I	le Ser 85	His	Leu	His	Ser	Leu 90	Phe	Arg	Val	Leu	Leu 95	Met	
Ser His		Ser Phe	Cys	Ala	Ser	His 105	Val	Ile	Lys	His	Phe 110	Phe	Cys	
Asp Thr	Gln P 115	ro Val	Leu	Lys	Leu 120	Ser	Cys	Ser	Asp	Thr 125	Ser	Ser	Ser	
Gln Met 130	Val V	al Met	Thr	Glu 135	Thr	Leu	Ala	Val	Ile 140	Val	Thr	Pro	Phe	
Leu Cys 145	Ile I	le Phe	Ser 150	Tyr	Leu	Arg	Ile	Ile 155	Ile	Thr	Val	Leu	Arg 160	

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Ile Pro Phe Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser
                165
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aat atc cag aca cac agc aaa gtc atc acc ttt gca qqc tqc atc acc
                                                                       97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
            20
                                25
cag ata ggc cat tgc cta ctc ttt gca gta ttg gac gtc ttt atg ctg
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Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac cca ctg cac
                                                                      193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
                        55
tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca
                                                                      241
Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
                    70
tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg
                                                                      289
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
                85
                                    90
ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tqc
                                                                      337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Cys
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385

gaa ctt aat cag gtc atc cac ctt gcc tgt tct gac act ttt ctt aat

Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn

120

115

gat gtg gtg atg tat ttg gcc gct gtg ctg ctg ggg ggt ggt ccc ctt Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Pro Leu 130 135	433
gca ggg att ctt tac tct tac tct aag ata gtt tcc tcc ata cgt gca Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160	481
atc tca tca gct cag ggg aag tac aag gca ttt tcc acc tgt gta tct Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165 170 175	529
cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190	577
ctt agt tot got goa act ggc aac toa cat toa aga got goa goo tog Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser 195 200 205	625
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Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 10 15 15 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr	AT 127070
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 15 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 25 Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu	AT 12/0/0
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 1 10 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 25 Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu 40 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His	AT 12/0/0
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 1 15 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 25 Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu 40 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala	T 12/0/0
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 15 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 25 Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu 40 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 80 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val	T 12/0/0

130 135 140	
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160	
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165 170 175	
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190	
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Val Met Tyr Thr Val Val Thr Pro 210 215	
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ned Arg ned	tcc ttc Ser Phe 100											337
gat gtt ctc Asp Val Leu 115												385
aaa atc gtg Lys Ile Val 130			Thr									433
tct gga atc Ser Gly Ile 145												481
gta tca cct Val Ser Pro												529
cac ctc tca His Leu Ser	gtg gtc Val Val 180	acc ctc Thr Leu	ttc Phe	tat Tyr 185	ggc Gly	acg Thr	ggc Gly	ctt Leu	999 Gly 190	gta Val	tat Tyr	577
ctc agt ctt Leu Ser Leu 195												625
gtg atg tac Val Met Tyr 210			Pro									649
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Leu A	rg Leu	Ser 100	Phe	Cys	Thr	Asn	Met 105	Glu	Ile	Pro	His	Phe 110	Phe	Cys	
Asp V	al Leu 115		Val	Leu	Lys	Leu 120	Ala	Cys	Ser	Glu	Thr 125	Leu	Val	Asn	
Lys I 1	le Val 30	Met	Tyr	Phe	Val 135	Thr	Ile	Ala	Met	Gly 140	Val	Phe	Pro	Leu	
Ser G 145	ly Ile	Leu	Tyr	Ser 150	Tyr	Ser	Gln	Ile	Phe 155	Ser	Ser	Ile	Leu	Arg 160	
Val S	er Pro	Ala	Gln 165	Gly	Gln	His	Lys	Ala 170	Phe	Ser	Thr	Cys	Gly 175	Ser	
His L	eu Ser	Val 180	Val	Thr	Leu	Phe	Tyr 185	Gly	Thr	Gly	Leu	Gly 190	Val	Tyr	
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aac at Asn II	tt caa le Gln	act Thr 20	cac His	agc Ser	aga Arg	gtc Val	atc Ile 25	gcc Ala	tat Tyr	gca Ala	agc Ser	tgc Cys 30	ctg Leu	aca Thr	97
cag at Gln Me	ig tot et Ser 35	ttt Phe	tca Ser	atc Ile	ttt Phe	ttt Phe 40	gtg Val	tgt Cys	atg Met	gaa Glu	gac Asp 45	atg Met	ctc Leu	ctt Leu	145
gct gt Ala Va 50	g atg al Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	cct Pro	ctg Leu	cac His	193

tat Tyr 65	cca Pro	gtc Val	atc Ile	atg Met	agc Ser 70	cca Pro	cga Arg	ctc Leu	tgt Cys	ggc Gly 75	ttc Phe	tta Leu	gtg Val	ttg Leu	gtg Val 80	241
tct Ser	gct Ala	ttt Phe	ctt Leu	agc Ser 85	ctt Leu	tta Leu	ata Ile	tcc Ser	cag Gln 90	gtg Val	cac His	aat Asn	ttg Leu	att Ile 95	gtc Val	289
tta Leu	caa Gln	ttt Phe	tct Ser 100	tgc Cys	ttc Phe	aaa Lys	gat Asp	ata Ile 105	aag Lys	att Ile	tct Ser	aat Asn	ttc Phe 110	ttc Phe	tgt Cys	337
gac Asp	cct Pro	tct Ser 115	caa Gln	ctc Leu	ctc Leu	aca Thr	ctt Leu 120	gct Ala	tgt Cys	tcc Ser	gac Asp	acg Thr 125	ttt Phe	gtc Val	aat Asn	385
aac Asn	aac Asn 130	ata Ile	gtc Val	atg Met	aat Asn	ttc Phe 135	ttt Phe	gct Ala	gct Ala	gta Val	ttt Phe 140	ggt Gly	ttt Phe	ctt Leu	ccc Pro	433
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aga Arg	gtt Val	cca Pro	tca Ser	tca Ser 165	agt Ser	gl ^à aaa	aag Lys	tat Tyr	aaa Lys 170	gcc Ala	ttc Phe	tct Ser	acc Thr	tgt Cys 175	agc Ser	529
tct Ser	cac His	ctg Leu	gca Ala 180	gtt Val	gtt Val	tgc Cys	tta Leu	ttt Phe 185	tat Tyr	gga Gly	aca Thr	gtc Val	ctt Leu 190	gga Gly	gtg Val	577
tac Tyr	ctt Leu	999 Gly 195	tca Ser	tca Ser	gtg Val	tca Ser	tcc Ser 200	ccc Pro	agg Arg	aag Lys	aga Arg	gtg Val 205	gtg Val	acc Thr	tca Ser	625
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Gln	Met	Ser 35	Phe	Ser	Ile		Phe 40	Val	Cys	Met	Glu	Asp 45	Met	Leu	Leu	
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Ser Ala Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
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Leu Gln Phe Ser Cys Phe Lys Asp Ile Lys Ile Ser Asn Phe Phe Cys
            100
Asp Pro Ser Gln Leu Leu Thr Leu Ala Cys Ser Asp Thr Phe Val Asn
Asn Asn Ile Val Met Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro
Ile Ser Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
Arg Val Pro Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser
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                                                       175
Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Leu Gly Val
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aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc
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Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
           20
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tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80	241
tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val 85 90 95	289
ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 100 105 110	337
gta ctt aat cag gtc atc cac ctt gcc tgt tct gac act ttt ctt aat Val Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125	385
gat gtg gtg atg tat ttg gcc gct gtg ctg ctg ggg ggt ggt ccc ctt Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Pro Leu 130 140	433
gca ggg att ctt tac tct tac tct aag ata gtt tcc tcc ata cgt gca Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160	481
atc tca tca gct cag ggg aag tac aag gca ttt tcc acc tgt gta tct Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165 170 175	529
cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190	577
ctt agt tct gct gca act ggc aac tca cat tca aga gct gca gcc tcg Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser 195 200 205	625
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Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Cys 100 105 110

Val Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Pro Leu 130 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190

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aat tt Asn Ph	t cta 1e Leu	tca Ser 20	gag Glu	aca Thr	aag Lys	gtt Val	atc Ile 25	tcc Ser	tac Tyr	atg Met	ggc Gly	tgc Cys 30	ctg Leu	gtc Val		97
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gcc to Ala Se 50	er Met	gcc Ala	atc Ile	gac Asp	cgg Arg 55	ctg Leu	gtg Val	gcc Ala	atc Ile	tgc Cys 60	aac Asn	ccc Pro	tta Leu	cac His		193
tat ga Tyr As 65	ıt gtg sp Val	gct Ala	atg Met	aac Asn 70	tcc Ser	cgg Arg	cgt Arg	tgc Cys	cta Leu 75	ctc Leu	atg Met	cta Leu	ttg Leu	ggt Gly 80		241
tct tg Ser Cy	gc agc 's Ser	atc Ile	tcc Ser 85	cac His	cta Leu	cat His	tcc Ser	ctg Leu 90	ttc Phe	cgg Arg	gtg Val	cta Leu	ctt Leu 95	atg Met		289
tct cg Ser Ar	g Leu	tct Ser 100	ttc Phe	tgt Cys	gcc Ala	tcc Ser	cac His 105	gtc Val	att Ile	aag Lys	cac His	ttt Phe 110	ttc Phe	tgt Cys		337
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cag at Gln Me 13	t Val	gtc Val	atg Met	act Thr	gag Glu 135	acc Thr	tta Leu	gct Ala	gtt Val	att Ile 140	gtg Val	acc Thr	ccc Pro	ttc Phe		433
ctg tg Leu Cy 145	t atc s Ile	atc Ile	ttc Phe	tcc Ser 150	tac Tyr	ctg Leu	cga Arg	atc Ile	atc Ile 155	atc Ile	act Thr	gtg Val	ctc Leu	aga Arg 160		481
atc cc Ile Pr	c tct o Ser	gca Ala	gcc Ala 165	gjå aaa	aag Lys	tgg Trp	agg Arg	gcc Ala 170	ttc Phe	tct Ser	acc Thr	tgt Cys	ggc Gly 175	tcc Ser		529
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Pro Met Tyr Phe Phe Met Ala Phe Ala Asn Thr Asp Ser Tyr Leu Leu

Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His

Tyr Asp Val Ala Met Asn Ser Arg Arg Cys Leu Leu Met Leu Leu Gly

Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met

Ser Arg Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys 105

Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 120

Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 135

Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg 150

Ile Pro Ser Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser 165

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<211> 649 <212> DNA

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cag Gln	att Ile	ttt Phe 35	ttt Phe	ttc Phe	gtt Val	gca Ala	ttt Phe 40	gga Gly	tgc Cys	ctg Leu	gac Asp	aat Asn 45	ttg Leu	ctc Leu	ttg Leu	145
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tac Tyr 65	gcg Ala	gtc Val	atc Ile	atg Met	aac Asn 70	ccc Pro	cgg Arg	ctc Leu	tgt Cys	aga Arg 75	ctg Leu	cta Leu	gtt Val	ctg Leu	80 GJÀ āāā	241
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gta Val	tca Ser	cct Pro	gcc Ala	caa Gln 165	ggc ggc	cag Gln	cac His	aaa Lys	gcc Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	999 Gly 175	tct Ser	529
cac His	ctc Leu	tca Ser	gtg Val 180	gtc Val	acc Thr	ctg Leu	ttc Phe	tat Tyr 185	ggc Gly	acg Thr	ggc Gly	ctt Leu	999 Gly 190	gta Val	tat Tyr	577
ctc Leu	agt Ser	tct Ser 195	gca Ala	gct Ala	aca Thr	cca Pro	tct Ser 200	tct Ser	agg Arg	aca Thr	agt Ser	ctg Leu 205	atg Met	gcc Ala	tcg Ser	625
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- Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
- Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly 75
- Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile 90
- Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Cys 105
- Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn 120
- Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu 130 135
- Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg 145 150
- Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
- His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
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cag Gln	att Ile	ttt Phe 35	ttt Phe	ttc Phe	gtt Val	gca Ala	ttt Phe 40	gga Gly	tgc Cys	ctg Leu	gac Asp	aat Asn 45	ttg Leu	ctc Leu	ttg Leu		145
acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttc Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His		193
tac Tyr 65	gcg Ala	gtc Val	atc Ile	atg Met	aac Asn 70	ccc Pro	cgg Arg	ctc Leu	tgt Cys	aga Arg 75	ctg Leu	cta Leu	gtt Val	ctg Leu	80 Gl 333		241
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aaa Lys	atc Ile 130	gtg Val	atg Met	tat Tyr	ttt Phe	gtg Val 135	aca Thr	att Ile	gca Ala	atg Met	ggt Gly 140	gtt Val	ttt Phe	cct Pro	ctc Leu		433
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gta Val	tca Ser	cct Pro	gcc Ala	caa Gln 165	ggc Gly	cag Gln	cac His	aaa Lys	gcc Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	999 Gly 175	tct Ser		529
cac His	ctc Leu	tca Ser	gtg Val 180	gtc Val	acc Thr	ctg Leu	ttc Phe	tat Tyr 185	ggc Gly	acg Thr	ggc Gly	ctt Leu	999 Gly 190	gta Val	tat Tyr		577
ctc Leu	agt Ser	tct Ser	gca Ala	gct Ala	aca Thr	cca Pro	tct Ser	tct Ser	agg Arg	aca Thr	agt Ser	ctg Leu	atg Met	gcc Ala	tcg Ser		625

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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly 70 75

Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile 85 90

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys 100 105

Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn 115

Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu 130

Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg

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cetgteagtt gtttgettat tttatggaac aggeatatgg gggtacetea gtteagatgt
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gac atg caa act cac agc aga gtc atc tcc tat gca ggc tgc ctg act
                                                                      97
Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
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tac Tyr 65	cca Pro	gtt Val	acc Thr	atg Met	aac Asn 70	cca Pro	tgt Cys	ttc Phe	tgt Cys	ggc Gly 75	ttc Phe	cta Leu	gtt Val	ttg Leu	ttg Leu 80		241
										ctg Leu							289
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gac Asp	ata Ile 130	gtc Val	atg Met	tat Tyr	ttc Phe	ctt Leu 135	gct Ala	gcc Ala	ata Ile	ttt Phe	ggt Gly 140	ttt Phe	ctt Leu	ccc Pro	atc Ile		433
ttg Leu 145	gjà aaa	atc Ile	ctt Leu	ttc Phe	tct Ser 150	tac Tyr	tat Tyr	aaa Lys	att Ile	gtt Val 155	tcc Ser	tcc Ser	att Ile	ctg Leu	agg Arg 160		481
gtt Val	tca Ser	tca Ser	tca Ser	ggt Gly 165	gly aaa	agg Arg	tat Tyr	aaa Lys	gcc Ala 170	ttc Phe	gcc Ala	acc Thr	tgt Cys	ggc Gly 175	tct Ser		529
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ctc Leu	agt Ser	tca Ser 195	gac Asp	atg Met	tcc Ser	tct Ser	tat Tyr 200	ccc Pro	aga Arg	aag Lys	ggt Gly	gca Ala 205	gtg Val	gct Ala	tca Ser		625
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20 25 30

Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp Asp Met Leu Leu 35 40

Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Pro Asp 50 60

Tyr Pro Val Thr Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu 65 70 75 80

Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile Ala 85 90 95

Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys
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Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn 115 120 125

Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro Ile 130 140

Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Phe Ala Thr Cys Gly Ser 165 170 175

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120

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cat	attg	cat	gttg	ıtgat	gc c	cttca	.ccaa	t aa	cato	atca	tgt	attt	ccc	tgtc	aacatg	420
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Gln Val Tyr Phe Leu 35	Met Met Phe Ala 40	Gly Met Asp		1
Ala Val Met Ala Tyr 50	Asp Arg Phe Val	Ala Ile Cys F	His Pro Leu Glr	1
Tyr Ala Val Ile Met 65	Asn Pro His Leu 70	Cys Gly Leu I 75	Leu Val Leu Ala 80	ì

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Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys 100 100 110

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His Leu Cys Val Val Ser Leu Phe Asn Gly Thr Gly Leu Gly Val Tyr
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Val Met Tyr Ala Met Val Thr Pro
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= AF127889
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Ile Met Ser Val Leu His Ser Leu Leu Gln Ser Leu Met Val

Leu Arg Leu Ser Leu Cys Arg Glu Leu Glu Ile Pro His Phe Cys

Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asp

Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Cys Leu

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Cys Ala 155

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser

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gct gta atg gcg tat gac cgc ttt gtg gcc atc tgc cac ccc ttg cac 193 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 55

tac gcc acg atc atg agc cca cgc ctc tgt ggc ctg ctg gtc ggg gcc 241 Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Ala 70

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70

75

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act Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	Asp	cgg Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tac Tyr	aca Thr	gtc Val	acc Thr	att Ile	aac Asn.	ccc Pro	aga Arg	ctg Leu	tgt Cys	gga Gly	ctg Leu	ctg Leu	gtt Val	ctg Leu	gca Ala	241

65	1				70					75					80		
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ct Le	g cgg	g ctt g Leu	tcc Ser 100	ttc Phe	tgc Cys	aca Thr	gac Asp	ttg Leu 105	Glu	atc Ile	ccc Pro	cgc Arg	ttt Phe 110	ttc Phe	tgc Cys	337	
ga Gl	a ctt u Leu	aat Asn 115	Gln	gtc Val	ata Ile	cat His	ctt Leu 120	gcc Ala	tgt Cys	tat Tyr	gac Asp	act Thr 125	ttc Phe	ctt Leu	aat Asn	385	
ga As	t gtg p Val 130	. Val	atg Met	tat Tyr	ttg Leu	gca Ala 135	gct Ala	atg Met	ctg Leu	ctg Leu	ggc Gly 140	ggt Gly	ggt Gly	ccc Pro	ctc Leu	433	
ac Th 14	a gga r Gly 5	att Ile	att Ile	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gca Ala 160	481	
at Il	c tca e Ser	tca Ser	gct Ala	cag Gln 165	Gly aaa	aag Lys	tac Tyr	aag Lys	gcg Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser	529	
ca Hi	c ato s Ile	tta Leu	att Ile 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	ggt Gly	aca Thr	ctc Leu	cta Leu	ggt Gly 190	gtg Val	tac Tyr	577	
ct Le	t agt u Ser	tct Ser 195	gct Ala	gca Ala	act Thr	ggc Gly	aac Asn 200	tca Ser	cat His	tca Ser	ggt Gly	gct Ala 205	gca Ala	gcc Ala	ttg Leu	625	
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Glı	ı Ile	Gly 35	His	Cys	Leu		Phe 40	Ala	Ala	Leu	Asp	Ile 45	Phe	Met	Leu		
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 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
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 Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
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 Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
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 Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
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 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
                  165
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
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aat atc cag aca cac agc aaa gtc atc acc ttt gca gac tgc atc acc
                                                                           97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Asp Cys Ile Thr
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25

cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu

		35					40					45					
	gtg Val 50																193
	aca Thr	_					-	_	_		_	_	-	_	_		241
	tgg Trp																289
_	cgg Arg				_		_	_	_						_		337
	ctt Leu																385
	gtg Val 130																433
_	gga Gly									_				_	-		481
	tca Ser																529
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Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
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Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys His Pro Leu His
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Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
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Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 120

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Pro Leu 135

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 150 155

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165

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Val Met Tyr Thr Val Val Thr Pro 210 215

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<223> Product = olfactory receptor

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cag Gln	ata Ile	ggc Gly 35	cat His	tgc Cys	cta Leu	ctc Leu	ttt Phe 40	gca Ala	gca Ala	ttg Leu	gac Asp	atc Ile 45	ttt Phe	atg Met	ctg Leu	145
act Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tac Tyr 65	aca Thr	gtc Val	acc Thr	att Ile	aac Asn 70	ccc Pro	aga Arg	ctg Leu	tgt Cys	gga Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gca Ala 80	241
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gaa Glu	ctt Leu	aat Asn 115	cag Gln	gtc Val	ata Ile	cat His	ctt Leu 120	gcc Ala	tgt Cys	tat Tyr	gac Asp	act Thr 125	ttc Phe	ctt Leu	aat Asn	385
gat Asp	gtg Val 130	gtg Val	atg Met	tat Tyr	ttg Leu	gca Ala 135	gct Ala	atg Met	ctg Leu	ctg Leu	ggc Gly 140	ggt Gly	ggt Gly	ccc Pro	ctc Leu	433
aca Thr 145	gga Gly	att Ile	att Ile	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gca Ala 160	481
atc Ile	tca Ser	tca Ser	gct Ala	cag Gln 165	gly ggg	aag Lys	tac Tyr	aag Lys	gcg Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser	529
cac His	atc Ile	tta Leu	att Ile 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	ggt Gly	aca Thr	ctc Leu	cta Leu	ggt Gly 190	gtg Val	tac Tyr	577
ctt Leu	Ser	tct Ser 195	gct Ala	gca Ala	act Thr	ggc Gly	aac Asn 200	tca Ser	cat His	tca Ser	agt Ser	gct Ala 205	gca Ala	gcc Ala	ttg Leu	625
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- Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
- Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
- Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
- Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val 90
- Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 100 105
- Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 115
- Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Pro Leu
- Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
- Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170
- His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
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- Val Met His Thr Val Val Thr Pro 210
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- <213> Saimiri sciureus
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- <223> Taxon = 9521; gene = SSC32; Accession DDBJ/EMBL/GenBank = AF127902

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cag Gln	gtg Val	tct Ser 35	ttt Phe	tca Ser	atc Ile	ttt Phe	ttt Phe 40	gcg Ala	tgt Cys	atg Met	gaa Glu	gac Asp 45	acg Thr	ctc Leu	ctg Leu	145
					gac Asp											193
tac Tyr 65	cca Pro	gtc Val	atc Ile	atg Met	aac Asn 70	cca Pro	cga Arg	ctc Leu	tgt Cys	ggc Gly 75	ttc Phe	tta Leu	gtg Val	ttg Leu	gtg Val 80	241
tct Ser	gtt Val	ttt Phe	ctt Leu	agc Ser 85	ctt Leu	tta Leu	ata Ile	tcc Ser	cag Gln 90	gtg Val	cac His	aat Asn	ttg Leu	att Ile 95	gtc Val	289
tta Leu	caa Gln	ttt Phe	tct Ser 100	tgc Cys	ttc Phe	aaa Lys	gag Glu	ata Ile 105	aag Lys	att Ile	tct Ser	aat Asn	ttc Phe 110	ttc Phe	tgt Cys	337
gac Asp	cct Pro	tct Ser 115	caa Gln	ctc Leu	ctc Leu	acc Thr	ctt Leu 120	tct Ser	tgt Cys	tct Ser	gac Asp	acc Thr 125	ttt Phe	gtc Val	aat Asn	385
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tca Ser 145	Gly 333	atc Ile	ttt Phe	ttc Phe	tct Ser 150	tac Tyr	tat Tyr	aaa Lys	att Ile	gcc Ala 155	tcc Ser	tcc Ser	att Ile	ctg Leu	aga Arg 160	481
gtt Val	cca Pro	tta Leu	tca Ser	agt Ser 165	Gly 999	aag Lys	tat Tyr	aaa Lys	gcc Ala 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	agc Ser 175	tct Ser	529
cac His	ctg Leu	gca Ala	gtt Val 180	gtt Val	tgc Cys	tta Leu	ttt Phe	tat Tyr 185	gga Gly	aca Thr	gtt Val	att Ile	gga Gly 190	gtg Val	tac Tyr	577
ctt Leu	Gly 333	tca Ser 195	tca Ser	atg Met	gca Ala	tcc Ser	ccc Pro 200	agg Arg	aag Lys	agt Ser	gtg Val	gtg Val 205	gcc Ala	tca Ser	gtg Val	625
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Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 65 70 75 80

Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 95

Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys 100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 120 125

Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130 135 140

Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg 145 150 155 160

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175

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Met Tyr Thr Val Val Thr Pro 210 215

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gtg g Val i	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tac Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	ctc Leu	ccc Pro	cta Leu	cat His	193
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tcc t Ser :	tgg Trp	gtg Val	ctg Leu	acc Thr 85	acc Thr	ttc Phe	cat His	gcc Ala	atg Met 90	ttg Leu	cac His	act Thr	tta Leu	ctc Leu 95	atg Met	289
gcc a Ala A																337
gat a Asp 1	atg Met	tct Ser 115	gct Ala	ctg Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gac Asp	act Thr 125	cga Arg	gtt Val	aat Asn	385
gaa t Glu 1																433
cta (Leu 1 145	ctt Leu	atc Ile	att Ile	Gly aaa	tcc Ser 150	tac Tyr	gca Ala	cga Arg	att Ile	gtc Val 155	ttc Phe	tcc Ser	atc Ile	ctc Leu	aag Lys 160	481
gtc (Val]	cct Pro	tct Ser	tct Ser	aag Lys 165	ggt Gly	atc Ile	tgc Cys	aag Lys	gcc Ala 170	gtc Val	tct Ser	act Thr	tgt Cys	ggc Gly 175	tcc Ser	529
cac (His I	ctc Leu	tct Ser	gtg Val 180	gtg Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	G1 ^A 333	act Thr	gtt Val	att Ile	ggt Gly 190	ctc Leu	tac Tyr	577
tta t Leu (tgc Cys	cca Pro 195	tca Ser	gct Ala	aat Asn	aat Asn	tct Ser 200	act Thr	cta Leu	aag Lys	gag Glu	act Thr 205	gtc Val	atg Met	gct Ala	625

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- Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His
- Tyr Ala Thr Ile Met Ser Pro Met Leu Ser Arg Ser Leu Val Ala Leu 75
- Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met 85
- Ala Arg Leu Arg Phe Cys Ala Asp Asn Val Ile Leu His Phe Phe Cys
- Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn 115
- Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Leu
- Leu Leu Ile Ile Gly Ser Tyr Ala Arg Ile Val Phe Ser Ile Leu Lys 150 155
- Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Val Ser Thr Cys Gly Ser 165 170
- His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr 180 185
- Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala 195 200

Val Met Tyr Thr Val Met Ala Pro 210 215

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cag at Gln Me															145
gct gt Ala Va 50	g atg l Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtt Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tac cc Tyr Pr 65															241
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tta ca Leu Gl															337
gac cc Asp Pr	t tct Ser 115	caa Gln	ctc Leu	ctc Leu	acc Thr	ctt Leu 120	tct Ser	tgt Cys	tct Ser	gac Asp	acc Thr 125	ttt Phe	gtc Val	aat Asn	385
aac at Asn Il 13	e Val														433
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gtt cc Val Pr															529

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Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 65 70 75 80	
Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 95	
Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys 100 105 110	
Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 120 125	
Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130 135 140	
Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg 145 150 155 160	
Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175	

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ggaagacaga agcatctcct tcacaggatg cgtcatgcaa ttcttttttg ccagcatatt
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tgtggtgaca gaaatattca tgctggcagt gatggcctat gacagatttg tggtggtgtg
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ttaccetetg ctctacacag ttgcaatgte ccagaggett ttetttttgt tagtggetae
                                                                     240
atcatacttc agggtgacag tetgtttett gacaattace ttetttetee tggaattate
                                                                     300
cttcagagga aataatatca ttaataactt tgtgtgtgag cctgctgcca ttgttgctgt
                                                                     360
gccatgcttt gacccctaca tgagccagga aatcattttc atttctgcca cattcaatga
                                                                     420
aacaagcagc ctgatgatca ttctcacctc ctaagatttc gtttttatca atgtcatgat
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gatgccttcc actgggggc gcataaaagc atgcgcgacc tgttcctccc agctgaccgc
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cattatcatt ttccatggga ccatctcttt tctctattgt gttcctaact ccaaaagttc
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P) 1	he Va	al A	sp I	le C	ys Va	al T	nr Se	er Tl	ar Tl		le P:	ro L	ys Tl	hr Le	eu Se:	r	
aac Asn	atc Ile	cag Gln	aca Thr 20	cac His	agc Ser	aaa Lys	gtc Val	atc Ile 25	acc Thr	tat Tyr	gca Ala	ggc	tgt Cys 30	gtc Val	acc Thr		97
cag Gln	ttg Leu	tac Tyr 35	ttt Phe	tct Ser	gta Val	ctc Leu	ttt Phe 40	ata Ile	Gly aaa	ttg Leu	gac Asp	agc Ser 45	tta Leu	ctc Leu	ctg Leu		145
acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cgc Arg		193
tac Tyr 65	atg Met	gtc Val	atc Ile	atg Met	aac Asn 70	cct Pro	cag Gln	ctc Leu	tgt Cys	gga Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gtg Val 80		241
tcc Ser	tgg Trp	atc Ile	atg Met	agt Ser 85	gcc Ala	ctg Leu	cat His	tcc Ser	ttg Leu 90	aca Thr	gaa Glu	agc Ser	tta Leu	atg Met 95	gca Ala		289
tta Leu	tca Ser	ctg Leu	ctc Leu 100	ttt Phe	tgt Cys	aca Thr	gac Asp	ttg Leu 105	aaa Lys	atc Ile	ctc Leu	cac His	ttt Phe 110	ttc Phe	tgt Cys		337
gaa Glu	ctt Leu	aat Asn 115	cag Gln	ata Ile	atc Ile	cac His	att Ile 120	gcc Ala	tgt Cys	tct Ser	gac Asp	acc Thr 125	tgt Cys	ctt Leu	aat Asn		385
aac Asn	ctg Leu 130	gtg Val	atg Met	tat Tyr	ttg Leu	tca Ser 135	gct Ala	gtg Val	ctg Leu	ctg Leu	ggc Gly 140	ggt Gly	ggt Gly	cct Pro	ctc Leu		433
gct Ala 145	Gly aaa	atc Ile	ctg Leu	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gct Ala 155	tcc Ser	tct Ser	ata Ile	cgt Arg	gca Ala 160		481
atc Ile	tca Ser	tca Ser	gct Ala	aag Lys 165	gly ggg	aag Lys	tac Tyr	aag Lys	gca Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser		529
cac His	ctc Leu	tca Ser	gtt Val 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	tgt Cys	aca Thr	ggc Gly	cta Leu	999 Gly 190	gtg Val	tac Tyr		577
ctg Leu	agt Ser	tct Ser 195	gct Ala	gca Ala	acc Thr	cac His	aac Asn 200	tca Ser	ctc Leu	tca Ser	agt Ser	aca Thr 205	gca Ala	gcc Ala	tcg Ser		625
gtg Val	atg Met 210	tac Tyr	act Thr	gtg Val	gtc Val	acc Thr 215	ccc Pro										649
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Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr 20 25 30

Gln Leu Tyr Phe Ser Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg 50 55 60

Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Val 65 70 75 80

Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Ala 85 90 95

Leu Ser Leu Leu Phe Cys Thr Asp Leu Lys Ile Leu His Phe Cys 100 105 110

Glu Leu Asn Gln Ile Ile His Ile Ala Cys Ser Asp Thr Cys Leu Asn 115 120 125

Asn Leu Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Pro Leu 130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala 145 150 155 160

Ile Ser Ser Ala Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser $165 \\ 170 \\ 175$

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr $180 \hspace{1cm} 185 \hspace{1cm} 190 \hspace{1cm}$

Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Ser Thr Ala Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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<211> 649

<212> DNA

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cag Gln	ata Ile	ggc Gly 35	cat His	tgc Cys	cta Leu	ctc Leu	ttt Phe 40	gca Ala	gca Ala	ttg Leu	gac Asp	atc Ile 45	ttt Phe	atg Met	ctg Leu	145
act Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tac Tyr 65	aca Thr	gtc Val	acc Thr	att Ile	aac Asn 70	ccc Pro	aga Arg	ctg Leu	tgt Cys	gga Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gca Ala 80	241
tcc Ser	tgg Trp	atc Ile	ctg Leu	agt Ser 85	gcc Ala	ctg Leu	aat Asn	tcc Ser	tca Ser 90	tta Leu	caa Gln	ccc Pro	tta Leu	ata Ile 95	gtg Val	289
ctg Leu	cgg Arg	ctt Leu	tcc Ser 100	ttc Phe	tgc Cys	aca Thr	gac Asp	ttg Leu 105	gaa Glu	atc Ile	ccc Pro	cac His	ttt Phe 110	ttc Phe	tgc Cys	337
gaa Glu	ctt Leu	aat Asn 115	cag Gln	gtc Val	ata Ile	cat His	ctt Leu 120	gcc Ala	tgt Cys	tat Tyr	gac Asp	act Thr 125	ttc Phe	ctt Leu	aat Asn	385
gat Asp	gtg Val 130	gtg Val	atg Met	tat Tyr	ttg Leu	gca Ala 135	gct Ala	atg Met	ctg Leu	ctg Leu	ggc Gly 140	ggt Gly	ggt Gly	ccc Pro	ctc Leu	433
aca Thr 145	gga Gly	att Ile	att Ile	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gca Ala 160	481
atc Ile	tca Ser	tca Ser	gct Ala	cag Gln 165	gly aaa	aag Lys	tac Tyr	aag Lys	gcg Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser	529
cac His	atc Ile	tta Leu	att Ile 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	ggt Gly	aca Thr	ctc Leu	cta Leu	ggt Gly 190	gcg Ala	tac Tyr	577
ctt Leu	agt Ser	tct Ser 195	gct Ala	gca Ala	act Thr	ggc Gly	aac Asn 200	tca Ser	cat His	tca Ser	agt Ser	gct Ala 205	gca Ala	gcc Ala	ttg Leu	625
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Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu 4.0

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Ala Tyr 180 185

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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       Product = olfactory receptor
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                                        10
ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
                                                                          97
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
             20
                                  25
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac
                                                                         145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
        35
aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
                                                                         193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
    50
gcc tgc tct gac act cga gtc aat gaa ttg gtg ata ttt atc atg gga
                                                                         241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca
                                                                         289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                                      90
cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc
                                                                         337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
            100
aag geg tte tet act tgt gge tee cae ete tet gtg gtg tea etg tte Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
                                                                         385
        115
tat ggg acc att att ggt ctc tac ttc tgc cca tca gct aat agt tct
                                                                         433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
act cta aag gag act gtt atg gct atg atg tac act gtg gtg acc ccc
                                                                         481
Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
                                          155
                                                               160
atg ctg
                                                                         487
Met Leu
<210> 148
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Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
            100
                                105
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
        115
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
    130
                        135
Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
145
Met Leu
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t gtt gcc atc tgc cag cct ctg cac tac tct acc ctc ttg agc cca tgg 49
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Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp 1 5 10 15
gcc tgc atg gcc atg gtg ggc acc tcc tgg ctc aca ggc atc atc acg Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr 20 25 30
gcc acc cat gcc ttc ctc atc ttc tct cta cct ttt ccc agc cgc Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg 35 40 45
cca atc atc cca cac ttt ctc tgt gac atc ctg cca gta ctg agg ctg Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu 50 55 60
gca agt gct ggg aag cac agg agc gag atc tct gtg atg aca gcc act Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr 65 70 75 80
gta gtc ttc att atg atc ccc ttc tct ctg att gtc acc tct tac atc Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile 85 90 95
cgc atc ctg gga gcc atc cta gcg atg gcc tcc acc cag agc cgc cgc 337 Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg 100 105 110
aag gtc ttc tcc acc tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc 385 Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe 115 120 125
ttt gga aca gcc agc atc acc tac atc cgg ccg cag gca ggc tcc tct Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser 130 135 140
gtt acc aca gac cgc gtc ctc agt gtg ttc tac acg gtc atc aca ccc 481 Val Thr Thr Asp Arg Val Leu Ser Val Phe Tyr Thr Val Ile Thr Pro 145 150 155 160
atg ct 486 Met
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Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr 20 25 30
Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg 35 40 45

<211> 482

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Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile
                                    90
Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
                            120
                                                125
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
                        135
Val Thr Thr Asp Arg Val Leu Ser Val Phe Tyr Thr Val Ile Thr Pro
145
                    150
                                        155
Met
<210> 151
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= 179718
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                                                                      60
actggctgct gcttcctggt tcccaggctt tcctgtagct actgtgcaga ccacgtggct
                                                                     120
cttcagcttt ccattctgtg gcaccaacaa ggtgaaccac ttcttctgtg acagcccacc
                                                                      180
tgtgctgaag ctggtctgtg tagacacagc actgtttgag atctacacca tcactggaac
                                                                      240
cattetggtg gtcatgatec cetgettget gatettgtgt teetacaete teattgetge
                                                                     300
tgccatcctc aagatcccat cagctaaagg gaagcataaa gccttctcta cgtgatcctc
                                                                     360
acateteett gttgtetete ttttetatet ateattaaae eteacatatt tteageetaa
                                                                      420
atcaaataat tctcctgaaa gcaaaaagct gctatcattg ttctacactg ttgtgactcc
                                                                     480
catgttg
                                                                     487
<210> 152
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= 179719
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                                                                       60
gctcctctgc ttgtgttggg ggctctctgt tctctatggt ctcctcctca ctctcctct
                                                                      120
gaccagggtg accttctgtg ggactcaaga gatccactac ctcttctgtg agatgtacgt
                                                                      180
cctgctgcag ctggcatgtt ccaacaccca catcattcac acaqtqctqq ttqctactqq
                                                                      240
ctgctttctt cctcgacccc ttagggttca cgactacatc ctatatacgt attgtcaqaa
                                                                      300
ccatccttca gataccctca gcctctaaga aacacaaaac cttctctgcc tgtgcctcac
                                                                      360
atttgggtgt ggtctccctc ttttatggga cacttgttat ggtatacctg cagccctcc
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acacctactc catgaaggac tcagtagcca cagtgatgta tgctgtggtg acacctatga
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tg
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tta tgc aca gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc att cat
                                                                       97
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His
ggg tot ato cag goo acc otg acc tto ogo ota coo tat tgt ggg occ
                                                                      145
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
                            40
                                                45
aat cag gta gat tac ttt atc tgt gac atc cct gca gta ttg aga ctg
                                                                      193
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
                        55
gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac atc
                                                                      241
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile
65
                    70
                                        75
                                                             80
gga gta gtg gcc gcc agt tgc ttc atg tta att cta ctt tcc tat qcc
                                                                      289
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Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
                85
                                    90
aac ata gtc cat gcc atc ctg aag ata cgc acc act gat ggg agg cgc
                                                                      337
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg
egg gee tte tet ace tgt gge tee cae eta act gtg gte aca gte tae
                                                                      385
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr
tat gtt ccc tgt att ttc atc tac ctt agg gct ggc tcc aag agc ccc
                                                                      433
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Pro
                        135
ctg gat ggg gca gtg gct gtg ttt tac act gtt gtc act cca ttc ctg
                                                                      481
Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu
                    150
                                        155
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Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arq Leu
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile
Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
                85
                                    90
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg
            100
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Pro
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Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu 145 150 155 160								
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ctg tgc atc cgg cta tta gtc ttg tca ttt gta ggt ggc ttc ctt cat Leu Cys Ile Arg Leu Leu Val Leu Ser Phe Val Gly Gly Phe Leu His 20 25 30	7							
gcc tta att cat gaa ggc att tta ttc aga tta acc ttc tgt aat tct Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser 35 40 45	5							
aac ata ata cat cac ttt tac tgt gac att atc cca ttg tta acg att 193 Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile 50 55 60	3							
tcc tgt act gac cct tct att aat ttt tta atg ctt ttt att ttg tct Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser 65 70 75 80	L							
ggt tca ata cag gta ttc act att ttg act gtt ctt gtc tct tat gca Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala 85 90 95	€							
ttt gtc ctc ttt aca atc tta aaa aaa aag tca gtc aaa ggc ata agg Phe Val Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Lys Gly Ile Arg 100 105 110	7							
aaa gcc ttt tcc acc tgt gga gcc cat ctc ttc tct gtc tgt tta tac 385 Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr 115 120 125	5							
tat ggc ccc ctt ctc ttc atg tat gtg ggc cct gca tct cca caa gca Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala 130 135 140	3							
gat gat caa gat atg gta gag tgt gta ttt tac act gtc atc att cct Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro 145 150 160	1							
ttc tta Phe Leu	7							

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<213> Papio hamadryas
<220>
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Leu Cys Ile Arg Leu Leu Val Leu Ser Phe Val Gly Gly Phe Leu His
Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser
                            40
Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile
Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser
Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala
Phe Val Leu Phe Thr Ile Leu Lys Lys Ser Val Lys Gly Ile Arg
                                105
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr
                            120
Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala
   130
                        135
Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro
145
                    150
Phe Leu
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ctc tgc ctc ctg ctg gtc tcc ctc aca tac ctc tat ggc ttt tct aca
Leu Cys Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr
                                25
gct att gtg gtt tca cct tgt ata ttc tct atg tct tat tgc tct tct
                                                                     145
Ala Ile Val Val Ser Pro Cys Ile Phe Ser Met Ser Tyr Cys Ser Ser
                            40
aat ata atc aat cat ttt tac tgt gat att gca cct ctg tta gca tta
                                                                     193
Asn Ile Ile Asn His Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu
tet tge tet gat act tae tta cea gaa gea ata gte tte ata tet gea
                                                                     241
Ser Cys Ser Asp Thr Tyr Leu Pro Glu Ala Ile Val Phe Ile Ser Ala
gca aca aat ttg gtt ttt tcc atg att aca gtt cta gta tct tat ttc
                                                                     289
Ala Thr Asn Leu Val Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe
                85
                                    90
aat att gtt ttg tcc att cta agg atg cat tca tca gaa gga agg aaa
                                                                     337
Asn Ile Val Leu Ser Ile Leu Arg Met His Ser Ser Glu Gly Arg Lys
            100
                                105
aaa gcc ttt tcc acc tgt gct tca cat atg atg gca gtc aca gtt ttc
                                                                     385
Lys Ala Phe Ser Thr Cys Ala Ser His Met Met Ala Val Thr Val Phe
                            120
tat ggg aca atg ctg ttc atg tat ttg cag ccc caa acc aac cac tca
                                                                     433
Tyr Gly Thr Met Leu Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser
   130
ctg gat act gat aag atg gct tct gtg ttt tac aca ttg gtg att cct
                                                                     481
Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro
atg ctg
                                                                     487
Met Leu
<210> 158
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<213> Papio hamadryas
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Leu Cys Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr
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                    4.0
       35
Asn Ile Ile Asn His Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu
Ser Cys Ser Asp Thr Tyr Leu Pro Glu Ala Ile Val Phe Ile Ser Ala
Ala Thr Asn Leu Val Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe
Asn Ile Val Leu Ser Ile Leu Arg Met His Ser Ser Glu Gly Arg Lys
                                105
Lys Ala Phe Ser Thr Cys Ala Ser His Met Met Ala Val Thr Val Phe
                            120
Tyr Gly Thr Met Leu Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser
    130
                        135
Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro
                                       155
                    150
145
Met Leu
<210> 159
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 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
                                                                       97
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgc gca gac
                                                                      145
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Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp

50 55 60	etg aag ctg 193 Jeu Lys Leu
gcc tgc tct gac act cga gtc aat gaa ttg gtg ata ttt a Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe I 65 70 75	
ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg t Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly S 85 90	— <u> </u>
cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag g Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys G 100 105	
aag geg tte tet act tgt gge tee cae ete tet gtg gtg t Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val S 115 120 125	
tat ggg acc att att ggt ctc tac ttc tgc cca tca gct a Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala A 130 135 140	
act cta aag gag act gtt atg ggt atg atg tac act gtg g Thr Leu Lys Glu Thr Val Met Gly Met Met Tyr Thr Val V 145 150 155	
atg ctg Met Leu	487
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100 105 110
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser 130 135 140
Thr Leu Lys Glu Thr Val Met Gly Met Met Tyr Thr Val Val Thr Pro 145 150 155 160
Met Leu
<210> 161 <211> 478 <212> DNA <213> Papio hamadryas
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t gtg gcc atc tgt aag ccc ttg aac tat gca acc atc atg agt caa cct Val Ala Ile Cys Lys Pro Leu Asn Tyr Ala Thr Ile Met Ser Gln Pro 1 5 10 15 atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
t gtg gcc atc tgt aag ccc ttg aac tat gca acc atc atg agt caa cct Val Ala Ile Cys Lys Pro Leu Asn Tyr Ala Thr Ile Met Ser Gln Pro 1 5 10 15 atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His 20 25 30 gga ggg atc cag act ctg ttc ata gcc cag tta cca ttc tgt ggc ccc Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro
t gtg gcc atc tgt aag ccc ttg aac tat gca acc atc atg agt caa cct Val Ala Ile Cys Lys Pro Leu Asn Tyr Ala Thr Ile Met Ser Gln Pro 1 5 10 15 atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His 20 25 30 gga ggg atc cag act ctg ttc ata gcc cag tta cca ttc tgt ggc ccc Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro 35 40 45 aat gtc atc gac cac ttt atg tgt gat tta gta cct ctt cta gag ctg Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
t gtg gcc atc tgt aag ccc ttg aac tat gca acc atc atg agt caa cct Val Ala Ile Cys Lys Pro Leu Asn Tyr Ala Thr Ile Met Ser Gln Pro 1 5 10 15 atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His 20 25 30 gga ggg atc cag act ctg ttc ata gcc cag tta cca ttc tgt ggc ccc Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro 35 40 45 aat gtc atc gac cac ttt atg tgt gat tta gta cct ctt cta gag ctg Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu 50 55 60 gcc tgc aca gac act cac acc ttg ggg cct ctg ata gct gcc aac agt Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser

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385
gct ctg tct agt tgt acc tct cat atc ttt gtt gtc atc tta ttc ttt
Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
                            120
                                                125
gtc cct tgt tca tac ctg tat cta aga cct cta acc tcc ttc ccc act
                                                                      433
Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Pro Thr
                        135
gac aaa gct gtg act gtg ttt tgc acc cta ttt aca cct atg ttg
                                                                      478
Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
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Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro
Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
            100
                                1.05
Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
                            120
        115
Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Pro Thr
                                             140
                        135
Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
                    150
                                         155
<210> 163
<211> 487
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<222> (2)..(487)
<223> Product = olfactory receptor
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gtc tgc aca ctg ctt gtt ttt act tct tgg ctg gtt tca ttc tta atc
                                                                       97
Val Cys Thr Leu Leu Val Phe Thr Ser Trp Leu Val Ser Phe Leu Ile
            2.0
ata ttc cca gca ctc atg ttg ctc tta cag ctt gat tac tgt agg tct
                                                                      145
Ile Phe Pro Ala Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Arg Ser
                            40
                                                                      193
aat att atg gac cat ttt acc tgt gat tat ttt ccc ctg ctg caa ctt
Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
                                             60
gct tgt tca gac aca aaa ttc cta gag gtg atg gga ttt tct tgt gct
                                                                      241
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala
gtg ttt act cta atg ttg act ttg gca tta ata ttt ctg tcc tac ata
                                                                       289
Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile
                85
tac att atc aga aca att ttg aga att cct tct gct agt caa agg aca
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr
                                 105
            100
aag gcc ttt tcc aca tgt tct tcc cac atg att gtc atc tcc atc tct
                                                                       385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
                            120
                                                 125
                                                                       433
tat ggc agc tgc att ttt atg tac att aaa ccc tca gca aaa gat aga
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
                        135
                                             140
qtq tcc ttq aqc aag gga gtg gca ata cta aac acc tca gta gcc ccc
                                                                       481
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Āla Pro
                     150
                                         155
atg ctg
                                                                       487
Met Leu
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Ile Phe Pro Ala Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Arg Ser
                           40
Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala
Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
                            120
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
                  150
Met Leu
<210> 165
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  Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp
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gcc Ala	tgc Cys	atg Met	gcc Ala 20	atg Met	gtg Val	ggc Gly	acc Thr	tcc Ser 25	tgg Trp	ctc Leu	aca Thr	ggc Gly	atc Ile 30	atc Ile	acg Thr	97
gcc Ala	acc Thr	acc Thr 35	cat His	gcc Ala	ttc Phe	ctc Leu	atc Ile 40	ttc Phe	tct Ser	cta Leu	cct Pro	ttt Phe 45	ccc Pro	agc Ser	cgc Arg	145
cca Pro	atc Ile 50	atc Ile	cca Pro	cac His	ttt Phe	ctc Leu 55	tgt Cys	gac Asp	atc Ile	ctg Leu	cca Pro 60	gta Val	ctg Leu	agg Arg	ctg Leu	193
gca Ala 65	agt Ser	gct Ala	G1 y 999	aag Lys	cac His 70	agg Arg	agc Ser	gag Glu	atc Ile	tct Ser 75	gtg Val	atg Met	aca Thr	gcc Ala	act Thr 80	241
gta Val	gtc Val	ttc Phe	att Ile	atg Met 85	atc Ile	ccc Pro	ttc Phe	tct Ser	ctg Leu 90	att Ile	gtc Val	acc Thr	tct Ser	tac Tyr 95	atc Ile	289
cgc Arg	atc Ile	ctg Leu	gga Gly 100	gcc Ala	atc Ile	cta Leu	gcg Ala	atg Met 105	gcc Ala	tcc Ser	acc Thr	cag Gln	agc Ser 110	cgc Arg	cgc Arg	337
aag Lys	gtc Val	ttc Phe 115	tcc Ser	acc Thr	tgc Cys	tcc Ser	tcc Ser 120	cat His	ctg Leu	ctc Leu	gtg Val	gtc Val 125	tct Ser	ctc Leu	ttc Phe	385
ttt Phe	gga Gly 130	Thr	gcc Ala	agc Ser	atc Ile	acc Thr 135	tac Tyr	atc Ile	cgg Arg	ccg Pro	cag Gln 140	gca Ala	ggc	tcc Ser	tct Ser	433
gtt Val 145	Thr	aca Thr	gac Asp	cgc Arg	gtc Val 150	ctc Leu	agt Ser	ctc Leu	ttc Phe	tac Tyr 155	Thr	gtc Val	atc Ile	aca Thr	ccc Pro 160	481
_	ctc Leu															487
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Ala	a Cys	s Met	20	a Met	. Val	. Gly	Thr	Ser 25	Tr	Leu	ı Thi	Gly	7 Il∈ 30	e Ile	e Thr	
Ala	a Thi	Th:	r His	s Ala	a Phe	e Lei	1 Ile 40	e Phe	e Sei	. Lei	ı Pro	Phe 45	e Pro	Sei	Arg	

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Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
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Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile
                85
Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg
                                105
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
                            120
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
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Val Thr Thr Asp Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro
                    150
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Met Leu
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  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
                                       10
                                                                       97
ctc tgt ctc tcc gtg gtg acg ctg tcc tgg gtg ctg acc acc ttc cat
Leu Cys Leu Ser Val Val Thr Leu Ser Trp Val Leu Thr Thr Phe His
                                 25
                                                                       145
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 aat gtg atc ccc cac ttt ttc tgt gat atg tct gct cta ctg aag ctg
                                                                       193
 Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 gcc tgc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga
                                                                       241
 Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
 65
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Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu

ggg ctc att gtt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 85 90 95	
aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105 110	
aag gcc ttg tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	
tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat agt tct Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser 130 135 140	
act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 145 150 155 160	
atg ctg Met Leu	
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115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser 130 135 140

Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 145 150 155

Met Leu

<210> 169 <211> 487 <212> DNA <213> Pan troglodytes
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gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 35 40 45
aat gtg atc ccc cac ttt ttc tgt gat atg tct gct cta ctg aag ctg Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 50 55 60
gcc tgc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly 70 75 80
ggg ctc att gtt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 85 90 95
aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105 110
aag gcc ttg tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc 385 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125
tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat agt tct Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser 130 135 140

act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 481 155 150 487 atg ctg Met Leu <210> 170 <211> 162 <212> PRT <213> Pan troglodytes <220> <221> misc_feature (1)...(487)<222> <223> Taxon = 9598; gene = PTR203; Accession DDBJ/EMBL/GenBank = AF179728 <400> 170 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly 70 Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 105 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser 135 130 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 155 150 145 Met Leu

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= AF179729
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                                                                      120
attgcgacta actttctgca ggtttaacat aatacattat ttctactgtg aaattttaca
                                                                      240
actgttcaaa atttcatgca atggtccatc tattaacgca ctaatgatat ttatttttgg
tgcttttata caaataccca ctttaatgac gatcataatc tcttatactc gtgtgctctt
                                                                      300
tgatattctg aaaaaaaagt ctgaaaaggg cagaagcaaa gccttctcca catgcagcgc
                                                                      360
ccatctgctt tctgtctcat tgtactacgg aactctgatc ttcatgtatg tgcgtcctgc
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tgcta
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 gtc tgt gcc cta atg ctt gca ttg tgc tgg gtc ctc acc aat atc att
                                                                        97
 Val Cys Ala Leu Met Leu Ala Leu Cys Trp Val Leu Thr Asn Ile Ile
             20
 gcc ctg act cac acg ttc ctc atg gct cgg ttg tcc ttc tgt gtg act
                                                                      145
 Ala Leu Thr His Thr Phe Leu Met Ala Arg Leu Ser Phe Cys Val Thr
         35
 ggg gaa att gct cac ttt ttc tgt gac atc act cct gtc ctg aag ctg
                                                                       193
 Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
 tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga
                                                                       241
 Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
                                         75
                     70
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ggc acc gta ctc atc gtc ccc ttt tta tgc att gtc acc tcc tac atc 289 Gly Thr Val Leu Ile Val Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile 85 90 95	
cac att gtg cca gct atc ctg agg gtc cga acc cgt ggt ggg gtg ggc His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Arg Gly Gly Val Gly 100 105 110	
aag gcc ttt tcc acc tgc agt tcc cac ctc tgc gtt gtt tgt gtg ttc Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Cys Val Phe 115 120 125	
tat ggg acg ctc ttc agt gcc tac ctg tgt cct ccc tcc att gcc tct Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser 130 135 140	
gaa gag aag gac att gca gca gct gca atg tac acc ata gtg act ccc Glu Glu Lys Asp Ile Ala Ala Ala Ala Met Tyr Thr Ile Val Thr Pro 145 150 155 160	
atg ttg Met Leu	
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Tyr	Gly 130	Thr	Leu	Phe	Ser	Ala 135	Tyr	Leu	Cys	Pro	Pro 140	Ser	Ile	Ala	Ser
Glu 145	Glu	Lys	Asp	Ile	Ala 150	Ala	Ala	Ala	Met	Tyr 155	Thr	Ile	Val	Thr	Pro 160

Met Leu

<210> 174 <211> 487 <212> DNA <213> Pan troglodytes	
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ctc tgt gcc tct ctg gta gct gca cct tgg gtc att gcc att Leu Cys Ala Ser Leu Val Ala Ala Pro Trp Val Ile Ala Ile 20 25 30	ttg aac 97 Leu Asn
cct ctc ttg cac act ctt atg atg gcc cat ctg cac ttc tgc Pro Leu Leu His Thr Leu Met Met Ala His Leu His Phe Cys 35 40 45	tct gat 145 Ser Asp
aat gtt atc cac cat ttc ttc tgt gat atc aac tct ctc ctc Asn Val Ile His His Phe Phe Cys Asp Ile Asn Ser Leu Leu 50 60	cct ctg 193 Pro Leu
tcc tgt tcc aac acc agt ctt aat cag ttg agt gtt ctg gct Ser Cys Ser Asn Thr Ser Leu Asn Gln Leu Ser Val Leu Ala 65 70 75	acg gtg 241 Thr Val 80
ggg ctg atc ttt gtg gta cct tca gtg tgt atc ctg gta tcc Gly Leu Ile Phe Val Val Pro Ser Val Cys Ile Leu Val Ser 85 90	tat atc 289 Tyr Ile 95
ctc att gtt tct gct gtg atg aaa gtc cct tct gcc caa gga Leu Ile Val Ser Ala Val Met Lys Val Pro Ser Ala Gln Gly 100 105 110	r Lys Leu
aag gct ttc tct atc tgt gga tct cac ctt gcc ttg gtc att Lys Ala Phe Ser Ile Cys Gly Ser His Leu Ala Leu Val Ile 115 120 125	ctt ttc 385 E Leu Phe
tat gga gca atc aca ggg gtc tat atg agc ccc tta tcc aat Tyr Gly Ala Ile Thr Gly Val Tyr Met Ser Pro Leu Ser Asr 130 135 140	cac tct 433 1 His Ser

act gaa aaa gac tca gcc gca tca gtc att ttt atg gtt gta gca cct Thr Glu Lys Asp Ser Ala Ala Ser Val Ile Phe Met Val Val Ala Pro 145 150 155 160
gtg ttg Val Leu
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Pro Leu Leu His Thr Leu Met Met Ala His Leu His Phe Cys Ser Asp 35 40 45
Asn Val Ile His His Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu 50 55 60
Ser Cys Ser Asn Thr Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val 65 70 75 80
Gly Leu Ile Phe Val Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile 85 90 95
Leu Ile Val Ser Ala Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu 100 105 110
Lys Ala Phe Ser Ile Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe 115 120 125
Tyr Gly Ala Ile Thr Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser 130 135 140
Thr Glu Lys Asp Ser Ala Ala Ser Val Ile Phe Met Val Val Ala Pro 145 150 155 160
Val Leu
<210> 176 <211> 487

<212 <213		NA an t	rogl	odyt	es											
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ctt Leu	tgc Cys	tcc Ser	ttg Leu 20	ttg Leu	gtg Val	gct Ala	aca Thr	tca Ser 25	tac Tyr	tgt Cys	tgg Trp	gly aaa	aga Arg 30	gtc Val	tgt Cys	97
tcc Ser	ctg Leu	aca Thr 35	ctt Leu	acc Thr	tac Tyr	ttt Phe	cta Leu 40	ctg Leu	gaa Glu	tta Leu	tcc Ser	ttc Phe 45	aga Arg	gga Gly	aat Asn	145
aat Asn	atc Ile 50	att Ile	aat Asn	aac Asn	ttt Phe	gtc Val 55	tgt Cys	gag Glu	cat His	gct Ala	gcc Ala 60	att Ile	gtt Val	gct Ala	gtg Val	193
tct Ser 65	tgc Cys	tct Ser	gac Asp	ccc Pro	tat Tyr 70	gtg Val	agc Ser	cag Gln	gag Glu	atc Ile 75	act Thr	tta Leu	gtt Val	tct Ser	gcc Ala 80	241
aca Thr	ttc Phe	aat Asn	gaa Glu	ata Ile 85	agc Ser	agc Ser	ctg Leu	gtg Val	atc Ile 90	act Thr	ctc Leu	act Thr	tcc Ser	tat Tyr 95	gct Ala	289
ttc Phe	att Ile	ttt Phe	atc Ile 100	act Thr	gtc Val	atg Met	aag Lys	acg Thr 105	gct Ala	tcc Ser	att Ile	Glà aaa	999 Gly 110	cgc Arg	aag Lys	337
aaa Lys	gcg Ala	ttc Phe 115	ttc Phe	acg Thr	tgt Cys	gcc Ala	tcc Ser 120	cac His	ttg Leu	acg Thr	gcc Ala	att Ile 125	acc Thr	att Ile	ttc Phe	385
cat His	999 Gly 130	Thr	att Ile	ctt Leu	ttc Phe	ctc Leu 135	Tyr	tgt Cys	gtt Val	cct Pro	aac Asn 140	Ser	aaa Lys	agt Ser	tcg Ser	433
tgg Trp 145	Leu	atg Met	gtc Val	aag Lys	gtg Val 150	Ala	tct Ser	gtc Val	ttt Phe	tac Tyr 155	Thr	gtg Val	gtc Val	att Ile	ccc Pro 160	481
_	ctg Leu															487
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Ser Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
                            40
Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
                        55
Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
                    70
Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Thr Leu Thr Ser Tyr Ala
                                    90
Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Ile Gly Gly Arg Lys
            100
Lys Ala Phe Phe Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Ser Ser
                         135
Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro
Met Leu
<210> 178
<211> 481
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 <221> CDS
 <222> (2)..(481)
 <223> Product = olfactory receptor
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Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg

10 97 tta tgc aca gtc ctt gtg gct gga gct tgt gtc gcc ggc tcc atg cat Leu Cys Thr Val Leu Val Ala Gly Ala Cys Val Ala Gly Ser Met His 2.0 ggg tot atc cag gcc acc ctg acc ttc cgc ctg ccc tac tgt ggg ccc 145 Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro 193 aat cag gtg gat tac ttt atc tgt gac atc ccc gca gta ttg aga ctg Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu 55 ged tgt get gad aca act gtd aat gag dtt gtg acd ttt gtg gad gtd 241 Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val ggg gtg gtg gcc gcc agt tgc ttc atg tta att ctg ctc tcg tat gcc 289 Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala 85 aac ata gta aat gcc atc ctg aag ata cgc acc act gat ggg agg cac 337 Asn Ile Val Asn Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg His 105 385 cgg gcc ttc tcc acc tgt ggc tcc cac cta atc gtg gtc aca gtc tac Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr 120 125 tat gtc ccc tgt att ttc atc tac ctt agg gct ggc tcc aaa ggc ccc 433 Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Gly Pro ctg gat ggg gcg gct gtg ttt tac act gtt gtc act cca tta ctg 481 Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu <210> 179 <211> 160 <212> PRT <213> Pan troglodytes <220> <221> misc_feature <222> (1)..(481) <223> Taxon = 9598; gene = PTR208; Accession DDBJ/EMBL/GenBank = AF179733 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg Leu Cys Thr Val Leu Val Ala Gly Ala Cys Val Ala Gly Ser Met His Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro

Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu

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Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
Asn Ile Val Asn Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg His
                                105
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
                            120
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Gly Pro
Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
<210> 180
<211> 487
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ctc tgt ggc ctg ctg gtt ctt gtg tcc tgg ttc ctc agc ttg tca tac
                                                                      97
Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
                                25
tcc ctg atc cag agt ctg ttg atg ctg cag gtg tcc ttc tgt acc agt
                                                                      145
Ser Leu Ile Gln Ser Leu Leu Met Leu Gln Val Ser Phe Cys Thr Ser
                            40
tgg gtc att cag cac ttt tac tgt gag ctt gct cag gtc ctc acg ctt
                                                                      193
Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu
    50
acc tgc tca gac aca cac gtc aat tac atc ctg ctg tac gtg gtg act
                                                                      241
Thr Cys Ser Asp Thr His Val Asn Tyr Ile Leu Leu Tyr Val Val Thr
ggc ctt ctg gac ttt gtg ccc ttc tca ggg atc ctt ttc tcc tac acc
                                                                      289
Gly Leu Leu Asp Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr
                                    90
caa att gtc tcc tac atc cta aga atc tca tcc aca gat ggg aaa cac
                                                                     337
Gln Ile Val Ser Tyr Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His
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Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val

100 105 110 aaa gcc ttt tct acc tgt gga tct cat ctg ttt gtg gtt tct tta ttc Lys Ala Phe Ser Thr Cys Gly Ser His Leu Phe Val Val Ser Leu Phe 385 120 tat ggg aca ggc ctt ggt gtg tat ctt agt tcc aat gca tcg tcc tct 433 Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser 135 tcc tgg tgg ggc atg gtg gcc tcg gtc atg tac act gtg gtc acc ccc Ser Trp Trp Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 481 150 155 atg ctg 487 Met Leu <210> 181 <211> 162 <212> PRT <213> Pan troglodytes <220> <221> misc_feature <222> (1)..(487) <223> Taxon = 9598; gene = PTR209; Accession DDBJ/EMBL/GenBank = AF179734 <400> 181 Val Ala Ile Cys His Pro Leu Tyr Tyr Arg Val Ile Val Asn Pro Arg 10 Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met Leu Gln Val Ser Phe Cys Thr Ser 40 Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu 55 Thr Cys Ser Asp Thr His Val Asn Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Asp Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Tyr Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His 105 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Phe Val Val Ser Leu Phe 120

Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser

135

ctg cta Leu Leu

Met Leu
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ctc agc gct cag ttg cta agc att tca tat gta att ggt ttc ctg cat 97 Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
20 25 30
cct ctg gtt cat gtg agt tta cta ttg cga cta act ttc tgc agg ttt 145 Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
35 40 45
aac ata ata cat tat ttc tac tgt gaa att tta caa ctg ttc aaa att 193 Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile 50 60
tca tgc aat ggt cca tct att aac gca cta atg ata ttt att ttt ggt 241 Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly
65 70 75 80
gct ttt ata caa ata ccc act tta atg acg atc ata atc tct tat tct 289 Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser
85 90 95
cgt gtg ctc ttt gat att ctg aaa aaa aag tct gaa aag ggc aga agc 337 Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
100 105 110
aaa gcc ttc tcc aca tgc agc gcc cat ctg ctt tct gtc tca ttg tac 385 Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr
115 120 125
tac gga act ctg atc ttc atg tat gtg cgt cct gca tct ggc tta gct 433 Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala 130 140
gaa gac cca gac aaa gtg tat tct ctg ttt tac acg att ata att ccc 481 Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
145 150 155 160

Ser Trp Trp Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 150

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<210> 183
<211> 162
<212> PRT
<213> Pan troglodytes
<220>
<221> misc feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR210; Accession DDBJ/EMBL/GenBank = AF179735
Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
                         55
Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly
Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser
                                     90
Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
                                 105
Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr
Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
    130
Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
Leu Leu
<210> 184
<211> 487
<212> DNA
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(487)
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<223> Taxon = 9598; gene = PTR211; Accession DDBJ/EMBL/GenBank = AF179736
<220>
<221>
      CDS
<222>
       (2)..(487)
     Product = olfactory receptor
<400> 184
t gtg gcc att tgc cac cca ctg agg tac aca gtc ctc atg aac atc cat
                                                                          49
  Val Ala Ile Cys His Pro Leu Arg Tyr Thr Val Leu Met Asn Ile His
ttc tgc ggc ttg ctg att ctt ctc tcc agg ttc atg agc act atg gat
                                                                          97
Phe Cys Gly Leu Leu Ile Leu Leu Ser Arg Phe Met Ser Thr Met Asp
            20
                                 25
gcc ctg gtt cag agt ctg atg ata ttt cag ctg tcc ttc tgc aaa aac
                                                                         145
Ala Leu Val Gln Ser Leu Met Ile Phe Gln Leu Ser Phe Cys Lys Asn
        35
                             40
gtt gaa ate eet tig tie tie tgt gaa gie git eag gie ate aag ete
                                                                         193
Val Glu Ile Pro Leu Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu
ged tgt tet gad acc etc atc aac atc etc ata tat tit gea agt
                                                                         241
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser
age ata ttt ggt gea att eet ete tet gga ata att tte tet tat tet
                                                                         289
Ser Ile Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser
                                      90
                                                                         337
caa ata gtc acc tct gtt ctg aga atg cca tca gca aga gga aag tat
Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr
                                 105
            100
aaa gcg ttt tcc acc tgt ggc tgt cac ctc tct gtt ttt tcc ttg ttc
                                                                         385
Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe
        115
tat ggg aca gct ttt ggg gtg tcc att agt tct gct gtt gct gag tct
                                                                         433
Tyr Gly Thr Ala Phe Gly Val Ser Ile Ser Ser Ala Val Ala Glu Ser
tcc cga att act gct gtg ggt tca gtg atg tac act gtg gtc cca caa Ser Arg Ile Thr Ala Val Gly Ser Val Met Tyr Thr Val Val Pro Gln \,
                                                                         481
                                                                         487
atg atg
Met Met
<210> 185
<211> 162
<212> PRT
<213> Pan troglodytes
<220>
<221> misc_feature
<222>
       (1)..(487)
<223> Taxon = 9598; gene = PTR211; Accession DDBJ/EMBL/GenBank = AF179736
Val Ala Ile Cys His Pro Leu Arg Tyr Thr Val Leu Met Asn Ile His
```

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Phe Cys Gly Leu Leu Ile Leu Leu Ser Arg Phe Met Ser Thr Met Asp 20 25 30
```

- Ala Leu Val Gln Ser Leu Met Ile Phe Gln Leu Ser Phe Cys Lys Asn 35 40 45
- Val Glu Ile Pro Leu Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu 50 55 60
- Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser 65 70 75 80
- Ser Ile Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser 85 90 95
- Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr $100 \hspace{1.5cm} 105 \hspace{1.5cm} 105$
- Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe 115 120 125
- Tyr Gly Thr Ala Phe Gly Val Ser Ile Ser Ser Ala Val Ala Glu Ser 130 140
- Ser Arg Ile Thr Ala Val Gly Ser Val Met Tyr Thr Val Val Pro Gln 145 150 155 160

Met Met

- <210> 186
- <211> 487
- <212> DNA
- <213> Pan troglodytes
- <220>
- <221> misc_feature
- <222> (1)..(487)
- <223> Taxon = 9598; gene = PTR212; Accession DDBJ/EMBL/GenBank = AF179737
- <220>
- <221> CDS
- <222> (2)..(487)
- <223> Product = olfactory receptor
- <400> 186
- t gtt gcc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag
 Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu

 1 5 10 15
- ctc tgt gtc ttc tta gtg gct gta tct tgg att ctg tct tgt gcc agc Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser 20 25 30

tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45
aac acc atc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg 193 Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg 241 Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc 289 Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95
tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 100 105 110
aaa gca ttg tcc aca tgt ggc tcc cat ctc tct gtg gtg tct ctc tat 385 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 115 120 125
tat ggg tca ata ttt ggc cag tac ctt ttc ccg act gta agc agt tct Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140
att gac aag gat gtc att gtg gct ctc atg tac acg gtg gtc aca ccc Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155 160
atg ttg Met Leu 487
<210> 187 <211> 162 <212> PRT <213> Pan troglodytes
<pre><220> <221> misc_feature <222> (1)(487) <223> Taxon = 9598; gene = PTR212; Accession DDBJ/EMBL/GenBank = AF179737</pre>
<400> 187 Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu 1 5 10 15
Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser 20 25 30
Ser Leu Ser His Thr Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60

```
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                    90
                                                        95
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
                            120
        115
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
                    150
                                        155
                                                             160
Met Leu
<210> 188
<211>
      484
       DNA
<212>
<213> Hylobates lar
<220>
<221> misc_feature
<222>
       (1)..(484)
<223> Taxon = 9580; gene = HLA121; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179738
<400> 188
                                                                       60
tgtggctatc tgcctgccgc ttaggtatcc agagctcatg agtgggcaga cctgcatgca
gatggcagca ctgagctggg ggacaggctt tgccaactca ctgctacagt ccatccttgt
                                                                      120
ctggcgcctc cctttctgtg gccacaacgt catcaaccac tttttctgtg agatcttggc
                                                                      180
agtgctaaaa ctggcctgtg gggacatctc cctcaatgcg ctggcattaa tggtggccac
                                                                      240
agetgteetg acaetggeee ecetettget catetgeetg tettacettt teatettgte
                                                                      300
tgccatcctt agggtaccct ctgctgcagg ccggcgcaaa gccttctcca cctgctcagc
                                                                      360
                                                                      420
ccacctcaca gtggtggtgg ttttttaagg gacaatttcc ttcatgtact tcaaacccaa
qqccaaqqac cccaacqtqq ataaqattqt tgcattgttg tatggggttg tgacaccctc
                                                                      480
gctg
                                                                      484
<210>
       189
<211>
       487
<212>
       DNA
<213> Hylobates lar
<220>
<221>
      misc feature
<222>
       (1)..(487)
<223> Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739
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<220>
<221> CDS
<222>
      (2)..(487)
      Product = olfactory receptor
<400> 189
t gtg gcg gtg tgt aac cct ctt ctc tac aca gtt gca atg tcc cag agg
  Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg
                                                                      97
ctt tgc tcc ttg ttg gtg gct aca tca tac tct tgg ggg ata gtc tgt
Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys
            20
                                25
ttc ctg aca ctt acc tac ttt cta ctg gaa tta tcc ttc aga gga aat
                                                                      145
Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
aat atc att aat aac ttt gtc tgt gag cat gcc att gtt gct gtg
                                                                      193
Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
tot tgc tct gac ccc tat gtg agc cag gag atc act tta gtt tct gcc
                                                                      241
Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
aca ttc aat gaa ata agc agt ctg atg att ttc act tcc tat gct
                                                                      289
Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala
                                    90
ttc att ttt atc act gtc atg aag atg cct tcc act ggg ggg cgc aag
                                                                      337
Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys
                                105
aaa gcg ttc tcc acg tgt gcc tcc cac ctg acc gcc att acc att ttc
                                                                      385
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
        115
cat ggg act atc ctt ttc ccc tac tgt gtt cct aac tcc aaa agt tca
                                                                      433
His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser
    130
                        135
tgg ctc atg gtc aag gtg acc tct gtc ttt tac aca gtg ttc att ccc
                                                                      481
Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro
145
                    150
                                        155
                                                            160
                                                                      487
atg gtg
Met Val
<210> 190
<211>
      162
<212> PRT
<213> Hylobates lar
<220>
<221> misc feature
       (1)..(487)
<223> Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739
<400> 190
Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg
```

Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys 25

Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn 40

Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val 50

Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala

Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala 90

Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys

Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe 120

His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser 130

Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro

Met Val

<210> 191 <211> 486

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 9580; gene = HLA123; Accession DDBJ/EMBL/GenBank = AF179740

<221> CDS

<222> (2)..(484)
<223> Product = olfactory receptor

t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 2.0

gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac 145 Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp

		35					40					45					
														aag Lys			193
														gca Ala			241
_		-		_				_	_	_	_	-		tat Tyr 95			289
														ata Ile			337
														atc Ile			385
														aac Asn			433
	_	-				-						-	_	act Thr			481
atg Met	tt																486
<210 <211 <212 <213	.> 1 2> I	192 161 PRT Hylok	oates	s lan	c												
<220 <221 <222 <223	L> 1	misc_ (1) Taxor	. (486	5)	; ger	ne =	HLA	123;	Acce	essio	on Di	OBJ/I	EMBL,	/GenI	3ank =	AF]	L7974(
<400 Val 1		192 Ile	Cys	His 5				Tyr		Thr	Ile	Met	Ser	Gln 15	Ser		
Gln	Cys	Val	Met 20	Leu	Val	Ala	Gly	Ser 25	Trp	Val	Ile	Ala	Cys 30	Ala	Cys		
Ala	Leu	Leu 35	His	Thr	Leu	Leu	Leu 40	Ala	Gln	Leu	Ser	Phe 45	Cys	Ala	Asp		
His	Ile 50	Ile	Pro	His	Phe	Phe 55	Cys	Asp	Leu	Gly	Ala 60	Leu	Leu	Lys	Leu		
Ser 65	Cys	Ser	Asp	Thr	Ser 70	Leu	Asn	Gln	Leu	Ala 75	Ile	Phe	Thr	Ala	Gly 80		

```
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                                    90
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
                            120
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
   130
                        135
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                    150
                                        155
Met
<210> 193
<211>
      487
<212> DNA
<213> Hylobates lar
<220>
<221> misc feature
<222> (1)..(487)
<223> Taxon = 9580; gene = HLA124; Accession DDBJ/EMBL/GenBank = AF179741
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 193
t gtg gcc atc tgt agt ccc ttg cac tac cca gtc atc atg aac caa agg
                                                                      49
 Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg
act cgt gcc aaa ctg gct gct gcc tcc tgg ttc cca ggc ttt cct gta
                                                                      97
Thr Arg Ala Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val
                                25
get act gtg cag acc aca tgg ctc ttc agt ttt cca ttc tgt ggc acc
                                                                     145
Ala Thr Val Gln Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr
                            40
aac aag gta aac cac ttc ttc tgt gac agc ccg cct gtg ctg agg ctg
                                                                     193
Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu
   50
gtc tgt gca gac aca gca ctg ttt gag atc tac gcc atc gtc gga acc
                                                                     241
Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr
att ctg gtg gtc atg atc cct tgc ttg ctg atc ttg tgt tcc tat act
                                                                     289
Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr
```

cac att gct gct atc ctc aag atc cca tcg gct aaa ggg aag aat

His Ile Ala Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn

	_			_	_				~	~		ctt Leu		385
				_								aat Asn		433
		~ ~	_	_	-		_		Thr	-	~ ~	act Thr		481
atg Met	ttg Leu													487

<210> 194

<211> 162 <212> PRT <213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA124; Accession DDBJ/EMBL/GenBank = AF179741

<400> 194

Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg

Thr Arg Ala Lys Leu Ala Ala Ser Trp Phe Pro Gly Phe Pro Val 20

Ala Thr Val Gln Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr

Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu

Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr

Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr

His Ile Ala Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn 105

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe

Tyr Ile Ser Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser 130 140

Met Leu	
<210> 195 <211> 487 <212> DNA <213> Hylobates lar	
<pre><220> <221> misc_feature <222> (1)(487) <223> Taxon = 9580; gene = HLA125; Accession DDBJ/EMBL/GenBank = AFI</pre>	179742
<220> <221> CDS <222> (2)(487) <223> Product = olfactory receptor	
<pre><400> 195 t gtg gcc atc tgc aag cct ctg cat tac ttg aat atc atg aat cga aga Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg 1 5 10 15</pre>	49
gtc tgc ata ctg ctt gtt ttt act tct tgg ctg att tca ttc tta atc Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile 20 25 30	97
ata ttc cct gca ctc atg ttg ctc tta aag ctt gat tac tgt agg tct Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser 35 40 45	145
aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg caa ctt Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu 50 55 60	193
gct tgt tca gac aca aaa ttc tta gag gtg atg gca ttt tct tgt gct Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala 65 70 75 80	241
gtg ttt act cta atg ttc act ttg gca tta ata tct ctg tcc tac ata Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile 85 90 95	289
tac att atc aga aca att ttg aga att cct tct act agt cag agg aca Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr 100 105 110	337
aag gcc ttt tcc aca tgt tct tcc cac atg gtt gtt att tcc atc tct Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser 115 120 125	385
tat ggc agc tgc att ttt atg tac att aaa ccc tca gca aaa gat aga Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 130 135 140	433
gtg tcc ttg agc aag gga gtg gca ata cta aac acc tca gta gcc ccc Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro 145 150 155 160	481
atg atg Met Met	487

Pro Glu Gly Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro 145 150 155 160

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<210> 196
<211> 162
<212> PRT
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9580; gene = HLA125; Accession DDBJ/EMBL/GenBank = AF179742
Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile
                                 25
Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser
Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala
Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile
                85
                                     90
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
            100
                                 105
Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
   130
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
Met Met
<210> 197
<211> 484
<212> DNA
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(484)
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<223> Taxon = 9580; gene = HLA126; Accession DDBJ/EMBL/GenBank = AF179743
<220>
<221> CDS
<222> (2)..(484)
<223> Product = olfactory receptor
t gtt gcc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag
                                                                       49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
                                      10
ctc tgt gtc ttc tta gtg gct ata tct tgg att ctg tct tgt gcc agc
                                                                       97
Leu Cys Val Phe Leu Val Ala Ile Ser Trp Ile Leu Ser Cys Ala Ser
tee etc tet cae ace ett etc etg ace egg etg tet tte tgt get geg
                                                                      145
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
aac acc atc ccc cac gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg
                                                                      193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg
                                                                      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
                    70
                                        75
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc
                                                                      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                    90
tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac
                                                                      337
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
            100
aaa gcg tcc acg tgt ggc tcc cat ctt tct gtg gtg tct ctc tat tat
                                                                      385
Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
                            120
ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att
                                                                      433
Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg
                                                                      481
Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
                    150
                                        155
ttg
                                                                      484
Leu
<210> 198
<211> 161
<212> PRT
<213> Hylobates lar
<220>
<221> misc_feature
<222>
      (1)..(484)
<223> Taxon = 9580; gene = HLA126; Accession DDBJ/EMBL/GenBank = AF179743
<400> 198
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
```

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Leu Cys Val Phe Leu Val Ala Ile Ser Trp Ile Leu Ser Cys Ala Ser
                                25
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- Ser Leu Ser His Thr Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35
- Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
- Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
- Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
- Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
- Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120 125
- Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile 130
- Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met 145 150 155

Leu

- <210> 199
- <211> 487 <212> DNA
- <213> Hylobates lar
- <220>
- <221> misc_feature
- <222> (1)..(487)
- <223> Taxon = 9580; gene = HLA127; Accession DDBJ/EMBL/GenBank = AF179744
- <220>
- <221> CDS
- <222> (2)..(487)
- <223> Product = olfactory receptor
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- cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25

49

gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc tt Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Ph 35 40 45	e Cys Ala Asp
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ct His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Le 50 55 60	
tcc tgc tca gat acc tcc ctc aat cag ttg gca atc tt Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Ph 65 70 75	
ttg aca gcc att atg ctt cca ttc ttg tgc atc ctg gt Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Va 85 90	
cac att ggg gtc acc atc ctc cag att ccc tct acc aa His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Ly 100 105	
aaa gcc ttg tcc att tgt gga tcc cac ctc tca gtg gt Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Va 115 120 12	il Thr Ile Tyr
tat ggg aca att att ggt ctc tat ttt ctt ccc cca tc Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Se 130 135 140	
aat gac aag aac ata att gct tca gtg ata tac aca gt Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Va 145 150 155	-
atg ttg Met Leu	487
<210> 200 <211> 162 <212> PRT <213> Hylobates lar	
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<pre><400> 200 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Me 1 5 10</pre>	et Ser Gln Ser 15
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Al 20 25	a Cys Ala Cys 30
Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Ph 35 40 45	
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Le 50 55 60	eu Leu Lys Leu
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Ph 65 70 75	ne Thr Ala Gly 80

85

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Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                85
                                    90
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
Met Leu
<210> 201
<211> 484
<212> DNA
<213> Hylobates lar
<220>
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  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
                                      10
ctc tgt gtc ttc tta gtg gct gta tct tgg att ctg tct tgt gcc agc
                                                                      97
Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
            20
                                25
tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg
                                                                     145
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
        35
aac acc atc ccc cac gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg
                                                                     193
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90

241

289

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 100 105 110
aaa gcg tcc acg tgt ggc tcc cat ctt tct gtg gtg tct ctc tat tat Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120 125
ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile 130 135 140
gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met 145 150 155 160
ttg Leu
<210> 202 <211> 161 <212> PRT <213> Hylobates lar
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<400> 202 Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu 1 5 10 15
Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser 20 25 30
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 100 105 110
Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120 125
Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile 130 135 140

Leu

<210> 203 <211> 484 <212> DNA <213> Hylobates lar	
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cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30	
gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40 45	
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60	
tcc tgc tca gat acc ttc ctc aat gag ctg gtc atg ttc aca gta ggg Ser Cys Ser Asp Thr Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 70 75 80	
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc 289 Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95	
tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac 337 Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 100 105 110	
aaa gcg tcc acg tgt ggc tcc cat ctt tct gtg gtg tct ctc tat tat 385 Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120 125	
ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att 433 Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile 130 135 140	

Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met 145 150 155 160

gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met

ttg 484 Leu <210> 204 <211> 161 <212> PRT <213> Hylobates lar <220> <221> misc_feature <222> (1)..(484) <223> Taxon = 9580; gene = HLA129; Accession DDBJ/EMBL/GenBank = AF179746 <400> 204 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser 1.0 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 40 His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 Ser Cys Ser Asp Thr Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120 Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile 130 Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met 145 150 155 Leu <210> 205 <211> 486 <212> DNA

<213> Hylobates lar

<220>

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= AF179747
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                                                                      60
ctggtggctg ggtcctgggt catcgcttgt gcgtgtgctc ttttgcatac cctcctcctg
                                                                     120
gcccagettt cettttgtgc tgaccacatc atccctcact tettetgtga cettggtgcc
                                                                     180
ctgctcaagt tgtcctgctc agatacctcc ctcaatcagt tggcaatctt tacagcagga
                                                                     240
ttgacagcca ttatgcttcc attcttgtgc atcctggttt cttatggtca cattggggtc
                                                                     300
accatectee agatteeete taccaaggge atatgeaaag eettgteeat ttgtggatee
cacctctcag tggtgactat ctattatggg acaattattg gtctctattt tcttccccca
                                                                     420
tecageaaca ecaatgacaa gaacataatt getteagtga tatacacagt agteacteec
                                                                     480
atgttg
                                                                     486
<210>
      206
<211>
       487
<212>
      DNA
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<221>
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<223> Taxon = 9580; gene = HLA131; Accession DDBJ/EMBL/GenBank = AF179748
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<222>
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<223> Product = olfactory receptor
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                                                                       49
  Val Ala Ile Cys Arg Pro Leu Tyr Tyr Pro Val Ile Met Lys Pro His
                  5
ctc tgt ggc ctg ctg gtt ctt gtg tcc tgg ttc ctc agc ttg tca tac
                                                                       97
Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
            20
tcc ctg atc cag agt ctg ttg atg ctg cgg gtg tcc ttc tgc acc agt
                                                                     145
Ser Leu Ile Gln Ser Leu Leu Met Leu Arg Val Ser Phe Cys Thr Ser
tgg gtc att cag cac ttt tac tgt gag ctt gct cag gtc ctc acg ctt
                                                                      193
Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu
                        55
                                            60
gcc tgc tca gac aca cac atc aat tac atc ctg ctc tac atg gtg acc
                                                                      241
Ala Cys Ser Asp Thr His Ile Asn Tyr Ile Leu Leu Tyr Met Val Thr
                    70
ggc ctt ttg ggc ttt gtg ccc ttc tca ggg atc ctt ttc tcc tac acc
                                                                      289
Gly Leu Leu Gly Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr
                85
                                    90
                                                        95
caa atc gtc tcc tcc atc ctg aga atc tca tcc cca gat ggg aaa cac
                                                                      337
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Gln Ile Val Ser Ser Ile Leu Arg Ile Ser Ser Pro Asp Gly Lys His 100 105 110	
aaa gcc ttt tct acc tgt gga tct cat ctg tct gtg gtt tct tta ttc Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	385
tat ggg aca ggt ctt ggc gtg tat ctt agt tcc aat gca tcg tcc tct Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser 130 135 140	433
tcc tgg cgg ggc atg gtg gct tcg gta atg tac act gtg gta acc ccc Ser Trp Arg Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155	481
aat gtg Asn Val	487
<210> 207 <211> 162 <212> PRT <213> Hylobates lar	
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Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr 20 25 30	
Ser Leu Ile Gln Ser Leu Leu Met Leu Arg Val Ser Phe Cys Thr Ser 35 40 45	
Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu 50 60	
Ala Cys Ser Asp Thr His Ile Asn Tyr Ile Leu Leu Tyr Met Val Thr 65 70 75 80	
Gly Leu Leu Gly Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr 85 90 95	
Gln Ile Val Ser Ser Ile Leu Arg Ile Ser Ser Pro Asp Gly Lys His 100 105 110	
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	
Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser 130 135	

atg ttg

Asn Val
<210> 208 <211> 487 <212> DNA <213> Hylobates lar
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cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30
gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40 45
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60
tcc tgc tca gat acc tcc ctc aat cag ttg gca atc ttt aca gca gga Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 70 75 80
ttg aca gcc att atg ctt cca ttc ttg tgc atc ctg gtt tct tat ggt Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95
cac att ggg gtc acc atc ctc cag act ccc tct acc aag ggc ata tgc His Ile Gly Val Thr Ile Leu Gln Thr Pro Ser Thr Lys Gly Ile Cys 100 105 110
aaa gcc ttg tcc att tgt gga tcc cac ctc tca gtg gtg act atc tat Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125
tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140
aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 155 160

Ser Trp Arg Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

487

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<210> 209
<211> 162
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<213> Hylobates lar
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Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
His Ile Ile Pro His Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
                         55
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                                   90
His Ile Gly Val Thr Ile Leu Gln Thr Pro Ser Thr Lys Gly Ile Cys
            100
                                 105
Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
                             120
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
                        135
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                     150
Met Leu
<210> 210
<211> 487
<212> DNA
<213> Gorilla gorilla
<220>
<221> misc_feature
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      (1)..(487)
<223> Taxon = 9593; gene = GGO100; Accession DDBJ/EMBL/GenBank = AF179750
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<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 210
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                                                                          49
 Val Ala Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn
                                                                          97
acc tgc att caa ctg gca gtt att tct tgg tcc agt agc ttc ctg tgt
Thr Cys Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Cys
tcc atg gtt atc aat gtt ctc acg ttg agt ttg ccc tac tgt ggg cct
                                                                         145
Ser Met Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro
                             40
aat atc ctg aat cac ttt ttc tgt gag gta cct act gtc ctg agg ttg
                                                                         193
Asn Ile Leu Asn His Phe Phe Cys Glu Val Pro Thr Val Leu Arg Leu
tct tgc acc gac acc tca ttc acg gag ctg gtt gtt ttt atc ttc agt Ser Cys Thr Asp Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser
                                                                         241
atc atc att gtc ttc atc cct ttc ctc ctc att gtt gtt tcc tat gtc
                                                                         289
Ile Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val
                85
                                      90
cgg atc ctt caa tct gtt ctc agg atg cgg tca gcc tcc ggg cgg tat
                                                                         337
Arg Ile Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr
            100
                                 105
                                                       110
aag gca tta tcc acc tgt acc tcc cat ttg aca gtg gta acc tta ttt
                                                                         385
Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe
        115
                             120
                                                  125
tat ggg act gcc atc ctc atg tac atg aga cca cag tcg agg tct tcc
                                                                         433
Tyr Gly Thr Ala Ile Leu Met Tyr Met Arg Pro Gln Ser Arg Ser Ser
    130
                         135
tgg get gge gge aag ate att geg gtt tte tac acg gtg gte aca eee
                                                                         481
Trp Ala Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro
atg ctt
                                                                         487
Met Leu
<210> 211
<211> 162
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<223> Taxon = 9593; gene = GG0100; Accession DDBJ/EMBL/GenBank = AF179750
<400> 211
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Val Ala Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn

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Thr	Сув	Ile	Gln	Leu	Ala	Val	Ile	Ser	Trp	Ser	Ser	Ser	Phe	Leu	Cys
			20					25					30		

Ser Met Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro 40

Asn Ile Leu Asn His Phe Phe Cys Glu Val Pro Thr Val Leu Arg Leu 55

Ser Cys Thr Asp Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser 70 75

Ile Ile Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val 85

Arg Ile Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr

Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe 120

Tyr Gly Thr Ala Ile Leu Met Tyr Met Arg Pro Gln Ser Arg Ser Ser

Trp Ala Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro 155

Met Leu

<210> 212

<211> 488

<212> DNA <213> Gorilla gorilla

<220>

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<222> (1)..(488)

<223> Taxon = 9593; gene = GGO101; pseudogene; Accession DDBJ/EMBL/GenBank = AF179751

<400> 212

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CCC	acct	gac a	agcto	gtcad	ec et	tctt	ctate	3 33	gcag	ccat	gtto	catc	tac (ctga	ggccta		420
ggc	gcta	ccg (ggcc	cccaç	gc ca	atgad	caago	g tg	gcct	ctat	ctto	ctaca	aca 🤅	gtcct	tactc		480
ccat	gct	3															488
<210 <211 <212 <213	1 > 4 2 > I	213 187 DNA Goril	lla q	goril	lla												
<220 <220 <220 <220	1> r 2>	(1).	_feat .(487 n = 9	7)	; gei	ne =	GGO:	102;	Acce	essio	on DI	OBJ/1	EMBL,	/GenI	3ank =	AF1	79752
<220 <220 <220 <220	1> (2>	_	.(48 ⁻ uct =		acto	ory 1	recer	otor									
	t gt									ır Va					aa gag lu Glu 5		49
ttc Phe	tgt Cys	gtc Val	ttc Phe 20	tta Leu	gtg Val	gct Ala	gta Val	tct Ser 25	tgg Trp	att Ile	ctg Leu	tct Ser	tgt Cys 30	gcc Ala	agc Ser		97
tcc Ser	ctc Leu	tct Ser 35	cac His	acc Thr	gtt Val	ctc Leu	ctg Leu 40	acc Thr	cag Gln	ctg Leu	tct Ser	ttc Phe 45	tgt Cys	gct Ala	gcg Ala		145
							tgt Cys										193
tcc Ser 65	tgc Cys	tca Ser	gat Asp	atc Ile	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 Gly 333		241
gtg Val	gtg Val	gtc Val	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggt Gly		289
tac Tyr	att Ile	gly aaa	gcc Ala 100	acc Thr	atc Ile	ctg Leu	gly ggg	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	ggg Gly 110	atc Ile	cac His		337
aaa Lys	gca Ala	ttg Leu 115	tcc Ser	aca Thr	tgt Cys	ggc Gly	tcc Ser 120	cat His	ctc Leu	tct Ser	gtg Val	gtg Val 125	tct Ser	ctc Leu	tat Tyr		385
						_	tac Tyr			_		_	_	_			433
att Ile 145	gac Asp	aag Lys	gat Asp	gtc Val	att Ile 150	gtg Val	gct Ala	ctc Leu	atg Met	tac Tyr 155	acg Thr	gtg Val	gtc Val	aca Thr	ccc Pro 160		481
acg	ttg																487

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<210> 214
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Ser Leu Ser His Thr Val Leu Leu Thr Gln Leu Ser Phe Cys Ala Ala
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
Tyr Ile Gly Ala Thr Ile Leu Gly Val Pro Ser Thr Lys Gly Ile His
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
        115
                             120
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Phe
                         135
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
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                                         155
Thr Leu
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cctqaqcttc ccatattqcq qtqcacacqa gatcgatcac ttcttctgcg aggcccccgt
                                                                     180
qctqqttcat ttqqcttqtq ctqacacttc aqtcttcgaa aacgccatgt acatctgctg
                                                                      240
tgtgttaatg ctcctggtcc ccttttccct catcctgtcc tcctatggtc tcatcctcgc
                                                                     300
tgctgttctg cacatgcgct ctacagaagc ccgcaagaag gcctttgcca cctgctcttc
                                                                      360
acatttggct gtggtgggac tcttttatgg agctgccatt tttacctata tgagacccaa
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atcccacagg tccactaacc acgataaggt tgtgtcagcc ttctatagta tgttcacccc
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                                                                      488
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                                                                      120
teatecetea ettettetgt gaeettggtg eeetgeteaa gttgteetge teagaeacet
                                                                      180
ccctcaatca gttagcaatc tttacagcag gattgacagc cattatgctt ccattcctgt
                                                                      240
gcatcctggt ttcttatggt cacattgggg tcaccatcct ccagattccc tctaccaagg
                                                                      300
gcatatgcaa agcettgtcc acttgtggat cccacctctc agtggtgact atctattatg
                                                                      360
ggacaattat tggtctctat tttcttcccc catcctgcaa caccaatgac gagaacataa
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gtg tgt gtt gtg ctg ctg gta atg tcc tgg gtt gga gga ttt ctg cac Val Cys Val Val Leu Leu Val Met Ser Trp Val Gly Gly Phe Leu His
                                                                         97
tca gta ttt caa ctt agc att att tat ggg ctc cca ttc tgt ggc ccc
                                                                        145
Ser Val Phe Gln Leu Ser Ile Ile Tyr Gly Leu Pro Phe Cys Gly Pro
                             40
aat gtc att gat cac ttt ttc tgt gac atg tat ccc tta ttg aaa ctg
                                                                        193
Asn Val Ile Asp His Phe Phe Cys Asp Met Tyr Pro Leu Leu Lys Leu
                         55
gtc tgc act gac acc cat gtt att ggc ctc tta gtg gtg acc aat gga
Val Cys Thr Asp Thr His Val Ile Gly Leu Leu Val Val Thr Asn Gly
gga ctg tct tgc act att gtg ttt ctg ctc tta ctc atc tct tat ggt
                                                                        289
Gly Leu Ser Cys Thr Ile Val Phe Leu Leu Leu Ile Ser Tyr Gly
gtc atc ttg cac tct cta aag aaa ctt agt cag aaa ggg agg caa aaa
                                                                        337
Val Ile Leu His Ser Leu Lys Lys Leu Ser Gln Lys Gly Arg Gln Lys
                                 105
gcc ctc tca acc tgc agt tcc cac atc act gtg gtt gtc ttc ttt
                                                                        385
Ala Leu Ser Thr Cys Ser Ser His Ile Thr Val Val Phe Phe Phe
                             120
gtt cct tgt att ttt atg tat gct aga cct gct agg agc ttc ccc att
                                                                        433
Val Pro Cys Ile Phe Met Tyr Ala Arg Pro Ala Arg Ser Phe Pro Ile
                         135
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            20
                                 25
Ser Val Phe Gln Leu Ser Ile Ile Tyr Gly Leu Pro Phe Cys Gly Pro
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Asn Val Ile Asp His Phe Phe Cys Asp Met Tyr Pro Leu Leu Lys Leu 50 55 60
Val Cys Thr Asp Thr His Val Ile Gly Leu Leu Val Val Thr Asn Gly 65 70 75 80
Gly Leu Ser Cys Thr Ile Val Phe Leu Leu Leu Leu Ile Ser Tyr Gly 85 90 95
Val Ile Leu His Ser Leu Lys Lys Leu Ser Gln Lys Gly Arg Gln Lys 100 105 110
Ala Leu Ser Thr Cys Ser Ser His Ile Thr Val Val Val Phe Phe 115 120 125
Val Pro Cys Ile Phe Met Tyr Ala Arg Pro Ala Arg Ser Phe Pro Ile 130 135 140
Asp Lys Ser Val Ser Val Phe Tyr Thr Val Ile Thr Pro Met 145 150 155
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att gca gtg ccc aca gcc ctc atc agt ggc ctg tcc ttc tgt ggc ccc 145 Ile Ala Val Pro Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro 35 40 45
cgt gcc atc aac cac ttc ttc tgt gac att gca ccc tgg att gcc ctg Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu 50 55 60
gcc tgc acc aac aca cag gca gta gag ctt gtg gcc ttt gtg att gct 241 Ala Cys Thr Asn Thr Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala 65 70 75 80

gtt gtg gtt atc ctg agt tca tgc ctc atc acc Val Val Val Ile Leu Ser Ser Cys Leu Ile Thr 85 90	
tac atc atc agc acc atc ctc agg atc ccc tct Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser 100 105	
aaa gcc ttc tcc acg tgc tcc tcg cat ctc acc Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr 115 120	
tat ggg tcc aca att ttc ctt cac gtc cgc acc Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr 130 135	
ttg gat ctg atc aaa gct gtc cac gtc ctg aac Leu Asp Leu Ile Lys Ala Val His Val Leu Asn 145 150 155	Thr Val Val Thr Pro
gtt tta a Val Leu	488
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	on DDBJ/EMBL/GenBank = AF179756
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<pre><223> Taxon = 9593; gene = GGO107; Accessi <400> 220 Leu Ala Ile Cys Tyr Pro Leu His Tyr Gly Ala 1</pre>	Met Met Ser Ser Leu 15 Cys Gly Phe Met Ala 30 Ser Phe Cys Gly Pro 45 Pro Trp Ile Ala Leu 60 Ala Phe Val Ile Ala 80
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Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp

115 120 125

Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala 130 135 140

Leu Asp Leu Ile Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro 145 150 155 160

Val Leu

<222>

<400> 222

(2)...(487)

<223> Product = olfactory receptor

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= AF179757
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                                                                     120
gaattateet teagaggaaa taatateatt aataaetttg tetgtgagea egetgteatt
                                                                     180
gttgctgtgt cttgctctga cccctatttg agccaggaga tcactttagt ttctgccaac
                                                                     240
attcaatgaa ataagcagcc tggtgatcat tctcacttcc tatgctttca tttttatcac
tgtcatgaag acgccttcca ctggggggcg caagaaagcg ttctccacqt gtgcctccca
cttgacggcc attaccattt tccatgggac tatccttttc ctctactgtg ttcctaactc
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49

97

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Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser His Ser

			20					25					30					
-		_		acc Thr			_	_					_	_	_		145	5
				cac His			_	_			_	_					19:	3
				acc Thr													24:	1
_		_		atg Met 85				_	_		_	_					28	€
			_	acc Thr			_					_			_		33'	7
	_	~		act Thr	_												38!	5
				att Ile													43	3
	_	_		ata Ile		_						_	_				48	L
atg Met	_																48	7
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Gln	Cys	Val	Met 20	Leu	Val	Ala	Gly	Ser 25	Trp	Val	Ile	Ala	Cys 30	Ala	Cys			
Ala	Leu	Leu 35	His	Thr	Leu	Leu	Leu 40	Ala	Arg	Leu	Ser	Phe 45	Cys	Ala	Asp			
His	Ile 50	Ile	Pro	His	Phe	Phe 55	Cys	Asp	Leu	Gly	Ala 60	Leu	Leu	Lys	Leu			

Ser 65	Cys	Ser	Asp	Thr	Ser 70	Leu	Asn	Gln	Leu	Ala 75	Ile	Phe	Thr	Ala	Gly 80	
Leu	Thr	Ala	Ile	Met 85	Leu	Pro	Phe	Leu	Cys 90	Ile	Leu	Val	Ser	Tyr 95	Gly	
His	Ile	Gly	Val 100	Thr	Ile	Leu	Gln	Ile 105	Pro	Ser	Thr	Lys	Gly 110	Ile	Cys	
Lys	Ala	Leu 115	Ser	Thr	Cys	Gly	Ser 120	His	Leu	Ser	Val	Val 125	Thr	Ile	Tyr	
Tyr	Gly 130	Thr	Ile	Ile	Gly	Leu 135	Tyr	Phe	Leu	Pro	Pro 140	Ser	Ser	Asn	Thr	
Asn 145	Asp	Lys	Asn	Ile	Ile 150	Ala	Ser	Val	Ile	Туг 155	Thr	Val	Val	Thr	Pro 160	
Met	Leu															
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_	a go			-						o Va	_	_	_		ac aa sn Ly 5	
		gct Ala		_		-				_				_		97
		gtt Val 35														145
	_	ata Ile					_					_				193
	-	aat Asn						_								241
gct	ttt	ata	caa	ata	ccc	act	tta	atg	act	atc	ata	atc	tct	tat	act	289

Ala Phe Ile Gln	Ile Pro Thr 85	Leu Met Thr I	Ile Ile Ile Ser	Tyr Thr 95
cgt gtg ctc ttt Arg Val Leu Phe 100	-	-		
aaa gcc ttc tcc Lys Ala Phe Ser 115				
tac gga act ctg Tyr Gly Thr Leu 130				
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ctg cta Leu Leu				487
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Val Ala Ile Cys Leu Ser Ala Gln 20 Pro Leu Val His	Leu Leu Ser Val Ser Leu	Ile Ser Tyr V 25 Leu Leu Arg I	Val Ile Gly Phe 30 Leu Thr Phe Cys 45	Leu His Arg Phe
Val Ala Ile Cys Leu Ser Ala Gln 20 Pro Leu Val His 35 Asn Ile Ile His	Leu Leu Ser Val Ser Leu Tyr Phe Tyr	Ile Ser Tyr V 25 Leu Leu Arg I 40 Cys Glu Ile I	Val Ile Gly Phe 30 Leu Thr Phe Cys 45 Leu Gln Leu Phe 60	Leu His Arg Phe Lys Ile
Val Ala Ile Cys Leu Ser Ala Gln 20 Pro Leu Val His 35 Asn Ile Ile His 50 Ser Cys Asn Gly	Leu Leu Ser Val Ser Leu Tyr Phe Tyr 55 Pro Ser Ile 70	Ile Ser Tyr V 25 Leu Leu Arg I 40 Cys Glu Ile I	Val Ile Gly Phe 30 Leu Thr Phe Cys 45 Leu Gln Leu Phe 60 Ile Ile Phe Ile	Leu His Arg Phe Lys Ile Phe Gly 80
Val Ala Ile Cys Leu Ser Ala Gln 20 Pro Leu Val His 35 Asn Ile Ile His 50 Ser Cys Asn Gly 65	Leu Leu Ser Val Ser Leu Tyr Phe Tyr 55 Pro Ser Ile 70 Ile Pro Thr 85	Ile Ser Tyr V 25 Leu Leu Arg I 40 Cys Glu Ile I Asn Ala Leu I Leu Met Thr I	Val Ile Gly Phe 30 Leu Thr Phe Cys 45 Leu Gln Leu Phe 60 Ile Ile Phe Ile 75 Ile Ile Ile Ser	Leu His Arg Phe Lys Ile Phe Gly 80 Tyr Thr 95

Tyr	Gly	Thr	Leu	Ile	Phe	Met	Tyr	Val	Arg	Pro	Ala	Ser	Gly	Leu	Ala
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Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro 145 150 150

Leu Leu

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tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45													
aac acc gtc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg Asn Thr Val Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60													
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 70 75 80													
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95													
tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 100 105 110													
aaa gca ttg tcc aca tgt ggc tcc cat ctc tct gtg gtg tct ctc tat Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 115 120 125													
tat ggg tca ata ttt ggc cag tac ctt ttc ccg act gta agc agt tct Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140													

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atg ttg Met Leu					487
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Ser Leu Ser 35	His Thr Leu	Leu Leu Th	nr Arg Leu	Ser Phe Cys 45	Ala Ala
Asn Thr Val	Pro His Val	Phe Cys As 55	sp Leu Ala	Ala Leu Leu 60	Lys Leu
Ser Cys Ser 65	Asp Ile Phe 70	Leu Asn Gl	iu Leu Val 75	Met Phe Thr	Val Gly 80
Val Val Val	Ile Thr Leu 85	Pro Phe Me	et Cys Ile 90	Leu Val Ser	Tyr Gly 95
Tyr Ile Gly	Ala Thr Ile	Leu Arg Va		Thr Lys Gly 110	Ile His
Lys Ala Leu 115	Ser Thr Cys	Gly Ser Hi 120	is Leu Ser	Val Val Ser 125	Leu Tyr
Tyr Gly Ser 130	Ile Phe Gly	Gln Tyr Le	eu Phe Pro	Thr Val Ser 140	Ser Ser
Ile Asp Lys 145	Asp Val Ile 150		eu Met Tyr 155	Thr Val Asp	Thr Pro 160
Met Len					

Met Leu

<210> 228

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ctc Leu	tgt Cys	ctc Leu	gcc Ala 20	ctg Leu	gtg Val	gcg Ala	ctg Leu	tcc Ser 25	tgg Trp	gtg Val	ctg Leu	acc Thr	acc Thr 30	ttc Phe	cat His	97
gcc Ala	atg Met	tta Leu 35	cac His	act Thr	tta Leu	ctc Leu	atg Met 40	gcc Ala	agg Arg	ttg Leu	tgt Cys	ttt Phe 45	tgt Cys	gca Ala	gac Asp	145
aat Asn	gtg Val 50	atc Ile	ccc Pro	cac His	ttt Phe	ttc Phe 55	tgt Cys	gat Asp	atg Met	tct Ser	gct Ala 60	ctg Leu	ctg Leu	aag Lys	ctg Leu	193
gcc Ala 65	ttc Phe	tct Ser	gac Asp	act Thr	cga Arg 70	gtt Val	aat Asn	gaa Glu	tgg Trp	gtg Val 75	ata Ile	ttt Phe	atc Ile	atg Met	gga Gly 80	241
glà aaa	ctc Leu	att Ile	ctt Leu	gtc Val 85	atc Ile	cca Pro	ttc Phe	cta Leu	ctc Leu 90	atc Ile	ctt Leu	Gly aaa	tcc Ser	tat Tyr 95	gca Ala	289
aga Arg	att Ile	gtc Val	tcc Ser 100	tcc Ser	atc Ile	ctc Leu	aag Lys	gtc Val 105	cct Pro	tct Ser	tct Ser	aag Lys	ggt Gly 110	atc Ile	tgc Cys	337
aag Lys	gcc Ala	ctc Leu 115	tct Ser	act Thr	tgt Cys	ggc Gly	tcc Ser 120	cac His	ctg Leu	tct Ser	gtg Val	gtg Val 125	tca Ser	ctg Leu	ttc Phe	385
tat Tyr	gga Gly 130	acc Thr	gtt Val	att Ile	ggt Gly	ctc Leu 135	tac Tyr	tta Leu	tgc Cys	tca Ser	tca Ser 140	gct Ala	aat Asn	agt Ser	tct Ser	433
act Thr 145	cta Leu	aag Lys	gac Asp	act Thr	gtc Val 150	atg Met	gct Ala	atg Met	atg Met	tac Tyr 155	act Thr	gtg Val	gtg Val	acc Thr	ccc Pro 160	481
	ctg Leu															487
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Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
Ala Phe Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
                     70
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser
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 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
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cctgctgaag cttgcctgta gtgaaaccag gccacgggaa tgggtgatct acctctcagc	240
ttttctggtc atcacaacca gcatttcagt gattcttaca tcgtacttgt tcatcattca	300
gtctattctg aagattcgta cagcaggtgg aaagccaaga ccttctccac ctgtgcttct	360
cacaagactg cattgactct cttctttgga acactcatat tcatatacct gaaaggcaac	420
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ggtgaaactg tetttetgtg ggecaaatgt cateagteae ttettetgtg atetteeece	180
actgttgaag ctgtcatgtt ctgagacatc tatgaatgaa ttgttgcttt tgatcttctc	240
tggcattatt gccacgctca cttttttgac tgtggtgatc tcctacatct tcattgttgc	300
tgctatcctg aggatccgct aagaagcagg tagacgtaaa gccttctcca cctgcacctc	360
tcacctgatt accgtgacct tattctatgg atcgataagc tttagttaca ttcagccaaa	420
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atgtttatgt cettttgtgg agacaacett gtcaatcact atatgtgtga cateetteet	180
-tt-range tetectors caretettac ataaatttgc togtgotttt tattattgtg	240

accgttggca	ttggggtgcc	gattgtcacc	atttttctct	cttatggttt	tattctttcc	300
agcattctcc	acattagttc	cacagagggc	aggtctaaag	ccttcagtac	ctgcagttcc	360
cacataattg	tggtatcgct	ttctttgggt	caggtgcttt	catgtacctc	aaaccacctt	420
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agcattctcc	acattagtto	cacagagggc	aggtctaaag	ccttcagtac	: ctgcagttcc	360
cacataattg	tggtatcgct	tttctttggg	ı tcaggtgctt	tcatgtacct	: caaaccacct	420
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att gtt cca cca ctt agc tta ggc ctc cag ctc gaa ttc tgt gac tcc Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser 35 40 45	
aat gcc att gat cat ttt agc tgt gat gca ggt cct ctc cta aag atc 193 Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile 50 55 60	
tca tgc tca gat aca tgg gta ata gaa cag atg gtt ata ctt atg gct Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala 70 75 80	
gta ttt gca ctc att atc acc cca gtt tgt gtg att ctg tcc tac ttg Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu 85 90 95	
tac ata gtc aga aca att ctg aag ttc cct tct gtt cag caa agg aaa Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys 100 105 110	
aag gcc ttt tct acc tgt tca tcc cac atg att gtg gtt tcc att gcc Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala 115 120 125	
tat gga agc tgc atc ttc atc tat atc aag ccc tct gca aaa gat gag Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu 130 135 140	
gtg gcc ata aat aaa gga gtt tca gtt ctt act act tct gtc gca ccc Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro 145 150 155 160	
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Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile	

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Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala
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Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu
Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys
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            100
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
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Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu
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                                                                       97
 ctc tgt gtc ttc tta gtg gct gta act tgg att ctg tct tgt gcc agc
 Leu Cys Val Phe Leu Val Ala Val Thr Trp Ile Leu Ser Cys Ala Ser
             20
 tee ete tet cae ace ett ete etg ace egg etg tet tte tgt get geg
                                                                      145
 Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
         35
 aac acc atc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg
                                                                      193
 Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg
                                                                      241
 Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
                     70
 gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc
                                                                      289
 Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
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85 90 95

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aaa gca ttg tcc Lys Ala Leu Ser 115	aca tgt Thr Cys	ggc tcc Gly Ser 120	cat cto	c tct gtg u Ser Val	gtg tct Val Ser 125	ctc t Leu T	at 385 Tyr
tat ggg tca ata Tyr Gly Ser Ile 130	ttt ggc Phe Gly	cag tac Gln Tyr 135	ctt tto Leu Pho	c ccg act e Pro Thr 140	. Val Ser	agt t Ser S	cct 433 Ser
att gac aag gat Ile Asp Lys Asp 145	gtc att Val Ile 150	gtg gct Val Ala	ctc atg Leu Me	g tac acc t Tyr Thi 155	g gtg gtc . Val Val	THT.	ccc 481 Pro 160
atg ttg Met Leu							487
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Leu Cys Val Ph 20		. Ala Val	l Thr T: 25	rp Ile Le	u Ser Cy 30	s Ala	Ser
							,
Ser Leu Ser Hi 35		ı Leu Le 40		rg Leu Se		s Ala	,
	s Thr Leu	40	u Thr A		er Phe Cy 45 la Leu Le		Ala
35 Asn Thr Ile Pi	s Thr Lev	40 L Phe Cy 55	u Thr A s Asp L	eu Ala A 6	er Phe Cy 45 la Leu Le O	u Lys	Ala
Asn Thr Ile Pr 50 Ser Cys Ser As	s Thr Leven His Value of the Photo 70	40 L Phe Cy 55 e Leu As	u Thr A s Asp L n Glu L ne Met C	eu Ala A 6 Leu Val M 75	er Phe Cy 45 la Leu Le O et Phe Th	u Lys nr Val	Ala Leu Gly 80
35 Asn Thr Ile Property Ser Cys Ser As Ser Cys Ser As Ser Val Val Val I	s Thr Let to His Value sp Ile Pho 70 le Thr Let 85	40 Phe Cy 55 Leu As	u Thr A s Asp L n Glu L ne Met C	eu Ala A. 60 Leu Val M 75 Cys Ile L	er Phe Cy 45 la Leu Le 0 et Phe Th eu Val Se hr Lys G	eu Lys ar Val er Tyr 95	Ala Leu Gly 80

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Met Leu
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catecagety cettletyty gycccaatga actygacaac ttetactyty atytectaca
                                                                      180
aatcatcaag ctggcctgca tggacaccta tgtggtagag gtgctggtga tagccaacag
                                                                      240
                                                                      300
tggtctgctg tctcttgtct gcttcttggt cttactattc tcttatgcta tcatcctgat
                                                                      360
caccetqaqa acacgettet gecagggeca gaacaaggte etetetacet gtgettetea
cctgacagtg gtcagcctga tcttcgtgcc atgcgtattc atctatttga ggcctttctg
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                                                                      120
tgcttcgtct gtccttctgt ggacccaatg acatcaacca cttttactgt gcggacccac
                                                                      180
ccctcttagt cctcgcctgc tcagatactt atgtcaaaga gaccgccatg ttggtggtgg
                                                                      240
ctggttccaa cctcatttgc tctctcaccg tcatcctcat ttcctacact ttcatcttca
                                                                      300
                                                                      360
ctgccattct gcgtatccac actgctgagg ggaggcgcaa ggccttctcc acctgcgggt
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Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser

130

ctca	tgtg	ac c	gctg	tcac	t gt	Cttc	tato	gga	icact	gtt	ctgc	atgt	ac c	etgag	gecee	420
cttc	tgag	ac a	ıtcta	ıtaca	a ca	9999	aaaa	ttg	gtago	tgt	tttt	tata	tc t	ttgt	gagtc	480
cgat	gtta															488
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	t go									ır Se					g aaa g Lys	
ctc Leu	tgc Cys	act Thr	cta Leu 20	ctt Leu	gtg Val	ctg Leu	tgt Cys	gcc Ala 25	tgg Trp	cta Leu	agt Ser	gjà aaa	ttt Phe 30	ctg Leu	acc Thr	97
														gct Ala		145
aac Asn	gtc Val 50	att Ile	gat Asp	cac His	ttt Phe	gca Ala 55	tgt Cys	gac Asp	tat Tyr	ttt Phe	ccc Pro 60	ctc Leu	tta Leu	caa Gln	cta Leu	193
tct Ser 65	tgt Cys	tca Ser	gat Asp	aca Thr	tgg Trp 70	ctc Leu	cta Leu	gaa Glu	gta Val	att Ile 75	ggt Gly	ttt Phe	tac Tyr	ttt Phe	gct Ala 80	241
ttg Leu	gtt Val	act Thr	ttg Leu	ctg Leu 85	ttc Phe	act Thr	ttg Leu	gca Ala	tta Leu 90	gtg Val	att Ile	tta Leu	tct Ser	tac Tyr 95	atg Met	289
tac Tyr	att Ile	atc Ile	agg Arg 100	acc Thr	att Ile	ttg Leu	aga Arg	atc Ile 105	ccg Pro	tct Ser	gcc Ala	agt Ser	caa Gln 110	aga Arg	aaa Lys	337
aag Lys	gct Ala	ttc Phe 115	tcc Ser	act Thr	tgt Cys	tct Ser	tct Ser 120	cac His	atg Met	att Ile	gtc Val	att Ile 125	tcc Ser	att Ile	tct Ser	385
														gaa Glu		433
gca Ala 145	tca Ser	ttg Leu	aca Thr	aaa Lys	gga Gly 150	ata Ile	gct Ala	att Ile	ctc Leu	aat Asn 155	aca Thr	tct Ser	gtt Val	gcc Ala	ccc Pro 160	481
atg Met	ctg Leu															487

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Asn Val Ile Asp His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu
Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala
Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
        115
                 120
Tyr Gly Ser Cys Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys
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                                      10
ctc tgt gca ctc atg ctg gcc atg tgc tgg ctg cta acc aac tgt cct
                                                                       97
Leu Cys Ala Leu Met Leu Ala Met Cys Trp Leu Leu Thr Asn Cys Pro
gca ttg atg cac acg ctg ttg ctg acc cgt gtg gct ttc tgt gcc cag
Ala Leu Met His Thr Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln
        35
agg gcc atc ccc cac ttc tac tgt gat ccc agt gct ctc ctg aag ctc
                                                                      193
Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu
gee tge teg gat ace ege ata aac gag etg atg ate ate gee atg gge
                                                                      241
Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly
ttg gcc ttc ctc acg gtt ccc ctc acg ctg atc gtc ttc tcc tac gtc
                                                                      289
Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val
                                    90
                85
                                                                      337
cgc atc tcc tgg gct gtg ctt ggc atc tcg tct cct gga ggg cga tgc
Arg Ile Ser Trp Ala Val Leu Gly Ile Ser Ser Pro Gly Gly Arg Cys
                                105
            100
aaa gcc ttc tcc acc tgt ggt tct cat ctc acg gtg gtt ctg ctc ttc
                                                                      385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe
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                            120
tat ggg tct ctt atg ggt gtg tat ttg ctt cct ccg tca tct tac tct
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Tyr Gly Ser Leu Met Gly Val Tyr Leu Leu Pro Pro Ser Ser Tyr Ser
                        135
                                                                      481
aca gag agg gaa agc agg gct gcc att ctc tac atg gtg atc att ccc
Thr Glu Arg Glu Ser Arg Ala Ala Ile Leu Tyr Met Val Ile Ile Pro
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Ala Leu Met His Thr Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln 35 40 45

Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu 50 60

Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly 65 70 75 80

Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val 85 90 95

Arg Ile Ser Trp Ala Val Leu Gly Ile Ser Ser Pro Gly Gly Arg Cys 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe 115 120 125

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Met

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cagtcagctt ccattctgtg acacccacat caaccacttc ttctgtgact atacacctct 180
aatggaggtg gtctgcagtg ggccaaaggt gctggagatg gtggatttta ccctggcctt 240
ggtggcaccg ctcagcacct tggtgctgat caccctgtcc tacatccaga tcatcagcac 300
gattgtcagg atcccctctg tccaggagag gaaaaaggct ttctccacct gttcctccca 360

tgtc	atcg	ita a	ittac	cato	it go	tatg	gaaa	gct	gttt	ttt	tatg	tatg	itc a	agco	ctccc	420	
cagg	rcaaa	igg 9	gttg	atct	a aa	caaa	ıggag	tgt	ctct	aat	caat	acag	rtt a	ttgc	cccc	480	
tctt	g															485	
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							gca Ala									97	
gct Ala	ttc Phe	tct Ser 35	ctc Leu	acc Thr	ctt Leu	ctg Leu	atg Met 40	act Thr	cag Gln	ttc Phe	tca Ser	ttc Phe 45	tgt Cys	gcc Ala	tcc Ser	145	
							tgt Cys									193	
gcc Ala 65	tgt Cys	tca Ser	gac Asp	acc Thr	cat His 70	atc Ile	ttt Phe	cag Gln	gtc Val	aca Thr 75	atg Met	tta Leu	act Thr	gaa Glu	gga Gly 80	241	
							ctt Leu									289	
							agg Arg									337	
							tct Ser 120									385	
							tat Tyr									433	
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atg	gtg															487	

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Cys Cys Leu Met Leu Val Ala Ala Ser Trp Leu Cys Ser His Cys Leu
Ala Phe Ser Leu Thr Leu Leu Met Thr Gln Phe Ser Phe Cys Ala Ser
His Ser Ile Gln His Phe Phe Cys Asp Val Pro Pro Leu Leu Lys Leu
Ala Cys Ser Asp Thr His Ile Phe Gln Val Thr Met Leu Thr Glu Gly
                    70
Val Leu Ser Gly Val Ile Pro Leu Thr Cys Val Leu Val Ser Tyr Ala
His Ile Met His Thr Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys His
Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe
                             120
Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser
Ala Asp Thr Gly Met Val Ala Cys Val Val Tyr Thr Met Val Thr Pro
Met Val
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<400> 248

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 Val Ala Ile Cys Lys Pro Leu His Tyr Val Ala Ile Met Ser Asn Thr
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                                                                            97
gtc tgc aga aga ctt gtc ttt tgt tgt tgg gta gct ggt ctg ttt att
Val Cys Arg Arg Leu Val Phe Cys Cys Trp Val Ala Gly Leu Phe Ile
                                                                           145
ata atc cct cca ctt agc ctg ggc cta aat ctg gaa ttt tgt gat tct
Ile Ile Pro Pro Leu Ser Leu Gly Leu Asn Leu Glu Phe Cys Asp Ser
                                                                           193
gat acc att gat cat ttt atc tgt gat gca tct ccc ctc ctg aat atc
Asp Thr Ile Asp His Phe Ile Cys Asp Ala Ser Pro Leu Leu Asn Ile
tot tgt tca aat act tgg ttc atg gaa cag act gtt atc atc tgt gca
                                                                           241
Ser Cys Ser Asn Thr Trp Phe Met Glu Gln Thr Val Ile Ile Cys Ala
                                                                            289
gtg ctg acc ctc att atg aca ctt atg tgt gta gtt ctg tcc tac att
Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile
                                                                           337
tat atc atc aag aca att tta gga ttc tct tct gcc cag caa aag aaa
Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys
             100
aaa gcc ttt tcc acc tgt tct tcc cac atg att gtg gtg tcc atc acc
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr
                                                                            385
                              120
        115
tat ggc agc tac atc ttc atc tat atc aaa cct tct gca aag gaa gaa
                                                                            433
Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu
                          135
    130
gta gcc att aac aag ggt gtg aca gtc ctc act act tcc atc gcc ccc Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro
                                                                            481
145
                                                                            487
atg ctg
Met Leu
<210> 248
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Val Ala Ile Cys Lys Pro Leu His Tyr Val Ala Ile Met Ser Asn Thr
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Val Cys Arg Arg Leu Val Phe Cys Cys Trp Val Ala Gly Leu Phe Ile
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Ile Ile Pro Pro Leu Ser Leu Gly Leu Asn Leu Glu Phe Cys Asp Ser 40

Asp Thr Ile Asp His Phe Ile Cys Asp Ala Ser Pro Leu Leu Asn Ile

Ser Cys Ser Asn Thr Trp Phe Met Glu Gln Thr Val Ile Ile Cys Ala

Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile 90 85

Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys 100 105

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr 115 120 125

Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu

Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro 150 155

Met Leu

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<213> Eulemur fulvus

20 25 30

	20		23	5		,	· ·		
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aat att att Asn Ile Ile 50	gac cat Asp His	ttt acc Phe Thr 55	tgt g Cys A	at tat sp Tyr	ttt ccc Phe Pro 60	ctg c Leu I	tg cag Leu Gln	ctt Leu	193
tcc tgt tca Ser Cys Ser 65	gat aca Asp Thr	aaa ttc Lys Phe 70	ctg g Leu G	ag ata lu Ile	atg ggg Met Gly 75	ttt t Phe S	cc tgt Ser Cys	gct Ala 80	241
gtg ttt act Val Phe Thr	cta atg Leu Met 85	ttc act Phe Thr	ttg g Leu A	ca tta la Leu 90	ata ttt Ile Phe	ctg t Leu S	cc tac Ser Tyr 95	atg Met	289
cac atc gtg His Ile Val	aga acg Arg Thr 100	att ttg : Ile Leu	Arg I	att cct lle Pro .05	tct act Ser Thr	Ser (cag agg Gln Arg 110	aca Thr	337
aag gcc ttt Lys Ala Phe 115	Ser Thr	tgt tct Cys Ser	tcc c Ser H	cac atg His Met	att gtc Ile Val	atc Ile 125	tcc atc Ser Ile	tct Ser	385
tat ggc ago Tyr Gly Ser 130	tgc att Cys Ile	ttt atg Phe Met 135	Tyr 1	att aag Ile Lys	ccc tca Pro Ser 140	Ala	aag gat Lys Asp	aga Arg	433
gta tct ttg Val Ser Leu 145	g agc aag 1 Ser Lys	g gca gtg s Ala Val 150	g gct g L Ala V	gtg cta Val Leu	atc acc Ile Thr 155	tca Ser	gta gct Val Ala	Pro 160	481
atg ctc Met Leu									487
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Val Cys Th	r Leu Le 20	eu Val Ph	e Ala	Ser Try 25	o Leu Va	l Ser	Phe Le 30	u Ile	
Val Phe Pr 35		eu Met Le	u Leu 40	Leu Ly	s Leu As	p Tyr 45	Cys Gl	y Phe	
Asn Ile Il 50	e Asp Hi.	is Phe Th 55		Asp Ty	r Phe Pr 60	o Leu	Leu Gl	n Leu	

Ser 65	Cys	Ser	Asp	Thr	Lys 70	Phe	Leu	Glu	Ile	Met 75	Gly	Phe	Ser	Cys	Ala 80	
Val	Phe	Thr	Leu	Met 85	Phe	Thr	Leu	Ala	Leu 90	Ile	Phe	Leu	Ser	Tyr 95	Met	
His	Ile	Val	Arg 100	Thr	Ile	Leu	Arg	Ile 105	Pro	Ser	Thr	Ser	Gln 110	Arg	Thr	
Lys	Ala	Phe 115	Ser	Thr	Cys	Ser	Ser 120	His	Met	Ile	Val	Ile 125	Ser	Ile	Ser	
Tyr	Gly 130	Ser	Cys	Ile	Phe	Met 135	Tyr	Ile	Lys	Pro	Ser 140	Ala	Lys	Asp	Arg	
Val 145		Leu	Ser	Lys	Ala 150	Val	Ala	Val	Leu	Ile 155	Thr	Ser	Val	Ala	Pro 160	
Met	Leu															
	1>	251 484 DNA Eule	emur	fulv	rus											
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<40)0> :aact	251 tatc	tqc	tatc	etc 1	taca	ctac	gg ga	acaa	tcate	g ago	cagc	ctgc	tgg:	ctgcaca	60
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															ttgcacc	180
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															ctcctct	360
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	tc															484
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                                       10
ctg gct aca cag ctg gcc ttg ggc tcc tgg gtc tgt ggt ttc ctg gcc
                                                                       97
Leu Ala Thr Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Leu Ala
                                 25
att gca gtg ctg acg gcc ctt atc agt ggc ctg tcc ttc tgt ggc gcc
                                                                       145
Ile Ala Val Leu Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Ala
        35
cgt gcc atc aac cac ttc ttc tgt gac att gca ccc tgg att gcc ctg
                                                                       193
Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu
gec tgc acc agc aca cag gca ata gag ctc gtg gcc ttt gtg att gct
                                                                       241
Ala Cys Thr Ser Thr Gln Ala Ile Glu Leu Val Ala Phe Val Ile Ala
                                         75
ttt gtg gtc atc ctg agt tca tgc ctc atc acc ctg gtc tcc tac gtg
                                                                       289
Phe Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val
                                     90
                 85
tac att atc agc acc atc ctc agg atc cca tct gcc agc ggc cgg agc
                                                                       337
Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser
             100
                                 105
aaa gcc ttc tct acg tgc tcc tct cac ctc acc gtg gtg ctc atc tgg
                                                                       385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp
                             120
         115
 tat ggg tee acg att ttt ett eat gte ege ace tee atc aca gae gee
                                                                        433
 Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Thr Asp Ala
                         135
 ttg gat ctg acc aaa gct gtc cat gtc ctg aac acc gtg gtg act cca
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 Leu Asp Leu Thr Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro
                                          155
                     150
                                                                        487
 gtt cta
 Val Leu
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Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu

Ala Cys Thr Ser Thr Gln Ala Ile Glu Leu Val Ala Phe Val Ile Ala 70

Phe Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val

Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser 105

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp 120

Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Thr Asp Ala 140

Leu Asp Leu Thr Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro 155

Val Leu

<210> 254

<211> 487

<212> DNA

<213> Eulemur fulvus

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<223> Product = olfactory receptor

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gtc tgc aca ctg ctc gtc ttt gcc tct tgg ctg gtt tca ttc tta atc

97

Val	Cys	Thr	Leu 20	Leu	Val	Phe	Ala	Ser 25	Trp	Leu	Val	Ser	Phe 30	Leu	Ile	
_			_			_			_	ctt Leu			_			145
			_				_	-		ttt Phe		_	-	_		193
	_		-				-			atg Met 75				_	_	241
										ata Ile						289
										tct Ser						337
_	_				_				_	att Ile	_					385
tat Tyr	ggc Gly 130	agc Ser	tgc Cys	att Ile	ttt Phe	atg Met 135	tac Tyr	att Ile	aag Lys	ccc Pro	tca Ser 140	gca Ala	aaa Lys	gat Asp	aga Arg	433
gta Val 145	tct Ser	ttg Leu	agc Ser	aag Lys	gca Ala 150	gtg Val	gct Ala	gtg Val	cta Leu	atc Ile 155	acc Thr	tca Ser	gta Val	gct Ala	ccc Pro 160	481
	ctc Leu															487
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Val	Cys	Thr	Leu 20	Leu	Val	Phe	Ala	Ser 25	Trp	Leu	Val	Ser	Phe 30	Leu	Ile	
Val	Phe	Pro 35	Ala	Leu	Met	Leu	Leu 40	Leu	Lys	Leu	Asp	Tyr 45	Cys	Gly	Phe	
Asn	Ile 50	Ile	Asp	His	Phe	Thr 55	Cys	Asp	Tyr	Phe	Pro 60	Leu	Leu	Gln	Leu	

Ser 65	Суз	Ser	Asp	Thr	Lys 70	Phe	Leu	Glu	Ile	Met 75	Gly	Phe	Ser	Cys	Ala 80	
Val	Phe	Thr	Leu	Met 85	Phe	Thr	Leu	Ala	Leu 90	Ile	Phe	Leu	Ser	Tyr 95	Met	
His	Ile	Val	Arg 100	Thr	Ile	Leu	Arg	Ile 105	Pro	Ser	Thr	Ser	Gln 110	Arg	Thr	
Lys	Ala	Phe 115		Thr	Cys	Ser	Ser 120	His	Met	Ile	Val	Ile 125	Ser	Ile	Ser	
Tyr	Gly 130		Cys	Ile	Phe	Met 135	Tyr	Ile	Lys	Pro	Ser 140	Ala	Lys	Asp	Arg	
Val		Leu	Ser	Lys	Ala 150	Val	Ala	Val	Leu	. Ile 155	Thr	Ser	Val	Ala	Pro 160	
Met	: Leu	ι														
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gt Va	~ +~	t ct s Le	c tt u Ph 20	c ct e Le	מ מכ	a tc a Se	t gg r Gl	c tg y Cy 25	s ir	g tt p Ph	c ct e Le	g gg u Gl	a to y Se 30	_ va	a gat 1 Asp	97
G]	jc tt y Ph	c at ie Me 35	t Le	c ac	t cc r Pr	a at o Il	c ac e Th 40	r Me	g ac et Th	c tt ir Ph	c cc e Pr	c ta o Ty 45	т сл	c ag	g tcc g Ser	145
co Ai	gg ga gg Gl 50	.u Il	t ca le Hi	c ca s Hi	ıt to .s Se	c tter Ph	те Сх	c ga s Gl	ia gt .u Va	c cc al Pr	t go o Al	.a va	a ac al Th	g ac ir Th	eg ctt ir Leu	193
t (Se 6!	er Cy	gc to ys Se	ca ga er As	ac ac sp Th	cc to nr Se 70	er Le	c ta eu Ty	it ga r Gl	aa at Lu Me	et Le	eu Me	g ta et Ti	ac ct yr Le	g to eu Cy	gc tgt ys Cys 80	241

gtc ctc atg ctc ctc att cct gtg aca gtc att tca agc tcc tat tca Val Leu Met Leu Leu Ile Pro Val Thr Val Ile Ser Ser Ser Tyr Ser 85 90 95	289
ttc att ctc ctc acc atc cac agg atg ggc tca gca gag ggc cgg aag Phe Ile Leu Leu Thr Ile His Arg Met Gly Ser Ala Glu Gly Arg Lys 100 105 110	337
aag gcc ttt gcc acc tgt tcc tcc cac atg acc gtg gtt atc ctc ttc Lys Ala Phe Ala Thr Cys Ser Ser His Met Thr Val Val Ile Leu Phe 115 120 125	385
tat ggg gcc gcc atc tac acc tac atg ctc ccc agc tcc tac cac act Tyr Gly Ala Ala Ile Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr 130 135 140	433
cct gag aag gac atg atg gtg tct gtc ttt tat acc atc cta act cct Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro 145 150 155 160	481
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115 120 125

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Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro 145 150 155 160

Val Leu

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tttaaatcta aaattctgtg actctaacat gattgatcat tttggttgcg atgcatttcc 180
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tcc ctc tcc cac acc ctt ctc ctg acc cgg ctg tcc ttc tgt gct gct Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45	145
aat gtc att ccc aac ttc ttc tgt gac ctt gct gct ctg ctc aag ctg Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60	193
tcc tgc tca gac atc ttc ctc aat gag ctg gtc atg ttt aca gta ggg Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80	241
gtg gtg gtc att acc ttg cca ttc tta tgt atc ctg gta tct tac ggc Val Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95	289
tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc tgc Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys 100 105 110	337
aaa gca tta tcc acg tgt ggg tcc cat ctc tct gtg gtg tct ctg tac Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 115 120 125	385
tac ggg gca ata ttt ggg cag tac ctt ttc cca gca tta agc aat tcc Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser 130 135 140	433
att gac aag gac atc att gtg gct atg atg tac acg gtg gtc aca ccc Ile Asp Lys Asp Ile Ile Val Ala Met Met Tyr Thr Val Val Thr Pro 145 150 160	481
atg ttg Met Leu	487

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Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
                             40
Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
                       55
    50
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
                     70
Val Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
 Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys
                                105
 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
                             120
 Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser
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ctg tgt cac ctt ctg gtg gct ggt tcc tgg ctg gga ggc ttt ctt cac
                                                                            97
Leu Cys His Leu Leu Val Ala Gly Ser Trp Leu Gly Gly Phe Leu His
tct att att cag att ttt atc acc atc caa tcg ccc ttt tgt ggt ccc
                                                                           145
Ser Ile Ile Gln Ile Phe Ile Thr Ile Gln Ser Pro Phe Cys Gly Pro
        3.5
                              40
                                                                           193
aac gtg att gac cac tac ttc tgt gac ctc ctg cca tta ttc aag ctt
Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu
                          55
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                                                                           241
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Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser
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ggc tta att ccc gtg tgc tcc ctg ttt atc ctg gtg tcc tcc tat atc
                                                                           289
Gly Leu Ile Pro Val Cys Ser Leu Phe Ile Leu Val Ser Ser Tyr Ile
                85
                                                                           337
att att ctg gtg cac ttg agg aaa cat tct gca gag ggg agg cac aaa
Ile Ile Leu Val His Leu Arg Lys His Ser Ala Glu Gly Arg His Lys
            100
                                  105
gcc ctc tct acc tgt gcc tct cac atc acg gtg gtc att ttg ttt ttt Ala Leu Ser Thr Cys Ala Ser His Ile Thr Val Val Ile Leu Phe Phe
                                                                           385
                              120
        115
gga cct gcc atc ttc ctc tac atg cga cct tcc tct acc ttc aca gaa
                                                                           433
Gly Pro Ala Ile Phe Leu Tyr Met Arg Pro Ser Ser Thr Phe Thr Glu
                          135
gac aaa ctc atg ggt gtg ttg tac aca gtc atc acc ccc agt
Asp Lys Leu Met Gly Val Leu Tyr Thr Val Ile Thr Pro Ser
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Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu

Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser

Gly Leu Ile Pro Val Cys Ser Leu Phe Ile Leu Val Ser Ser Tyr Ile 90

Ile Ile Leu Val His Leu Arg Lys His Ser Ala Glu Gly Arg His Lys 105

Ala Leu Ser Thr Cys Ala Ser His Ile Thr Val Val Ile Leu Phe Phe 120

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gca ata ata tta acc agc aac aca ttc acg ttg gat ttt tgt ggt gac 145 Ala Ile Ile Leu Thr Ser Asn Thr Phe Thr Leu Asp Phe Cys Gly Asp 35 40

193 aat qtc atc gac gac ttt ttc tgt gat gtc cca ccc ctg gtg aag ttg Asn Val Ile Asp Asp Phe Phe Cys Asp Val Pro Pro Leu Val Lys Leu 50 60 55

gcc tgt gat gtg gaa ggg agc tac cag gct gtg ctg tac ttc ctc Ala Cys Asp Val Glu Gly Ser Tyr Gln Ala Val Leu Tyr Phe Leu 65 70 75	_
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ttc atc atc gca gca gtc ttg agg gtc cgc tcc agc cgg ggc cgc Phe Ile Ile Ala Ala Val Leu Arg Val Arg Ser Ser Arg Gly Arg 100 105 110	
aag gcc ttc tcc acg tgc tcc tcc cac ctg atc tct gtt acc tta Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Ser Val Thr Leu 115 120 125	
tac ggc tcc att ctc tac atc tac tct cgc cca agt tcc agc tat Tyr Gly Ser Ile Leu Tyr Ile Tyr Ser Arg Pro Ser Ser Ser Tyr 130 135 140	
ctc gag agg gac aaa atg gtc tct acc ttt tac acc gtg ctg ttc Leu Glu Arg Asp Lys Met Val Ser Thr Phe Tyr Thr Val Leu Phe 145 150 155	ccc 481 Pro 160
acg ctc Thr Leu	487
<210> 267 <211> 162 <212> PRT <213> Eulemur rubriventer	
<pre><220> <221> misc_feature <222> (1)(487) <223> Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/Ge</pre>	nBank = AF179786
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<pre> <221> misc_feature <222> (1)(487) <223> Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/Ge <400> 267 Val Ala Ile Ser Asn Pro Pro Leu Tyr Val Gln Ala Met Pro Arg 1 5 10 15 Leu Cys Ile Cys Phe Ile Ile Cys Ser Tyr Thr Gly Gly Phe Val </pre>	Lys Asn
<pre> <221> misc_feature <222> (1)(487) <223> Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/Ge <400> 267 Val Ala Ile Ser Asn Pro Pro Leu Tyr Val Gln Ala Met Pro Arg 1</pre>	Lys Asn Asp
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Phe	Ile	Ile	Ala	Ala	Val	Leu	Arg	Val	Arg	Ser	Ser	Arg	Gly	Arg	Leu
			100					105					110		

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Ser Val Thr Leu Tyr \$115\$ \$120\$ \$125\$

Tyr Gly Ser Ile Leu Tyr Ile Tyr Ser Arg Pro Ser Ser Ser Tyr Ser 130 135 140

Leu Glu Arg Asp Lys Met Val Ser Thr Phe Tyr Thr Val Leu Phe Pro 145 150 155 160

Thr Leu

<210> 268 <211> 478 <212> DNA <213> Eulemur rubriventer <220> <221> misc_feature <222> (1)..(478) <223> Taxon = 34829; gene = ERU163; Accession DDBJ/EMBL/GenBank = AF179787 <220> <221> CDS <222> (2)..(478) <223> Product = olfactory receptor 49 t gtt gcc gta tgt aac cct ttg cat tac ctg acg gtc atg aac cgc cag Val Ala Val Cys Asn Pro Leu His Tyr Leu Thr Val Met Asn Arg Gln ctc tgc ctt cag ttg gtt ttt gcc tgc tgg tgt ggg ggt ttc atc cac Leu Cys Leu Gln Leu Val Phe Ala Cys Trp Cys Gly Gly Phe Ile His tot gtc aca cag gtt ata ctg gtc atc cag ctg ccc ttc tgt ggc ccc 145 Ser Val Thr Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro 40 193 aac aaa ttg gac agt ttc tac tgt gat gtc cca gag gtc atc aag ctg Asn Lys Leu Asp Ser Phe Tyr Cys Asp Val Pro Glu Val Ile Lys Leu 50 gcc tgc ctg gac acc tat gtg gta gaa gtg ctg atg gtt acc aac agt Ala Cys Leu Asp Thr Tyr Val Val Glu Val Leu Met Val Thr Asn Ser 241 289 ggt ctg cta tct ctt gtc tgc ttc ttg gtc ttg ata ttc tct tat gcc Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Ile Phe Ser Tyr Ala 337 acc atc ctg acc acc ctg aga act cgc ctc cac cag ggc cag agc aag Thr Ile Leu Thr Thr Leu Arg Thr Arg Leu His Gln Gly Gln Ser Lys

385

gcc ttc tct acc tgt gcc tcc cac cta atg gtg gtc agc ctg atc ttt Ala Phe Ser Thr Cys Ala Ser His Leu Met Val Val Ser Leu Ile Phe

gtg cca tgt gta ttc atc tac ttg agg cct ttc tgc agc ttc tct gtg 433 Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val 130 135

gat aag ata ttc tct gtg ttt tac atg gtg atc aca cct atg ttg 478 Asp Lys Ile Phe Ser Val Phe Tyr Met Val Ile Thr Pro Met Leu 150

<210> 269

<211> 159 <212> PRT <213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(478) <223> Taxon = 34829; qene = ERU163; Accession DDBJ/EMBL/GenBank = AF179787

<400> 269

Val Ala Val Cys Asn Pro Leu His Tyr Leu Thr Val Met Asn Arg Gln

Leu Cys Leu Gln Leu Val Phe Ala Cys Trp Cys Gly Gly Phe Ile His

Ser Val Thr Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro

Asn Lys Leu Asp Ser Phe Tyr Cys Asp Val Pro Glu Val Ile Lys Leu

Ala Cys Leu Asp Thr Tyr Val Val Glu Val Leu Met Val Thr Asn Ser

Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Ile Phe Ser Tyr Ala 85

Thr Ile Leu Thr Thr Leu Arg Thr Arg Leu His Gln Gly Gln Ser Lys 105

Ala Phe Ser Thr Cys Ala Ser His Leu Met Val Val Ser Leu Ile Phe 115 120

Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val

Asp Lys Ile Phe Ser Val Phe Tyr Met Val Ile Thr Pro Met Leu 155 150

<210> 270

<211> 487 <212> DNA

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<222> (2)..(487)
<223> Product = olfactory receptor
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  Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Ile Ser Thr Arg
                                                                           97
gtt tgt atc ctt ctt gtc tgt agc tcc tgg ctt gca gga ttc ttg atc
Val Cys Ile Leu Leu Val Cys Ser Ser Trp Leu Ala Gly Phe Leu Ile
                                                                          145
atc ttt cca cca ata atc ctt ctt ctg cag ttg gac ttc tgt gcc tcc
Ile Phe Pro Pro Ile Ile Leu Leu Gln Leu Asp Phe Cys Ala Ser
aat ata att gat cat ttt atc tgt gat tct tct cca att ctg cag ctt
                                                                          193
Asn Ile Ile Asp His Phe Ile Cys Asp Ser Ser Pro Ile Leu Gln Leu
 50
tct tgt aca aac act cac ttt cta gaa ctc atg gca ttt tgt tta gcc
                                                                          241
Ser Cys Thr Asn Thr His Phe Leu Glu Leu Met Ala Phe Cys Leu Ala
gtg gtg aca ctc atg gtc acc ttg acc tta gtt att ctc tcc tat aca
                                                                          289
Val Val Thr Leu Met Val Thr Leu Thr Leu Val Ile Leu Ser Tyr Thr
aat att atc cgg aca att cta aga att cct tct atg agt caa agg aaa
                                                                           337
Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys
aaa gee ttt tee act tgt tee tee cat ata ata gtt gtt tee ete tet
                                                                           385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile \bar{\text{Val}} Val Ser Leu Ser
        115
tat qqt aqt tqt atc ttc atq tac ata aag cct tct aca agg gaa agg
                                                                           433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg
gtg act tta agc aaa gga gta gct gtg gtt aat act tca gtg gct cct
Val Thr Leu Ser Lys Gly Val Ala Val Val Asn Thr Ser Val Ala Pro
                                                                           481
                                           155
                                                                           487
ctt ttq
Leu Leu
<210> 271
<211> 162
<212> PRT
<213> Eulemur rubriventer
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<221> misc_feature <222> (1)..(487)
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<223> Taxon = 34829; gene = ERU164; Accession DDBJ/EMBL/GenBank = AF179788 <400> 271

Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Ile Ser Thr Arg

Val Cys Ile Leu Leu Val Cys Ser Ser Trp Leu Ala Gly Phe Leu Ile 25

Ile Phe Pro Pro Ile Ile Leu Leu Leu Gln Leu Asp Phe Cys Ala Ser

Asn Ile Ile Asp His Phe Ile Cys Asp Ser Ser Pro Ile Leu Gln Leu

Ser Cys Thr Asn Thr His Phe Leu Glu Leu Met Ala Phe Cys Leu Ala

Val Val Thr Leu Met Val Thr Leu Thr Leu Val Ile Leu Ser Tyr Thr

Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Ser

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg

Val Thr Leu Ser Lys Gly Val Ala Val Val Asn Thr Ser Val Ala Pro 150 155

Leu Leu

<210> 272

<211> 483 <212> DNA

<213> Eulemur rubriventer

<220>

<221> misc feature

<222> (1)..(483)

<223> Taxon = 34829; gene = ERU165; pseudogene; Accession DDBJ/EMBL/GenBank = AF179789

<400> 272

cgttgccatc tgcaagcccc tccactaccc ccgtgctcat gagcagcagg gtctgcacac 60

ageteateet egeetgetgg etggeagggt teteetteat eattgtgeet gteateetga

ccagtcaget tecattetgt gacacceaea teaaccaett ettetgtgae tatacaeete

taatggaggt ggtctgcagt gggccaaagg tgctggagat ggtggatttt accctg	gcct 240
tggtggcact gctcagcacc ttggtgctga tcaccctgtc ctacatccag atcatc	agga 300
cgattgtcag gatcccctct gtccaggaga ggaaaaaggc tttctccacc tgttcc	tccc 360
atgtcatcgt ggttaccatg tgctatggaa gctgtttttt tatgtatgtc aagccc	tccc 420
caggcaaagg ggttgatcta aacaaaggag tgtcttaatc aatacaatta ttgccc	ccct 480
ctt	483
<210> 273 <211> 486 <212> DNA <213> Eulemur rubriventer <220> <221> misc_feature <222> (1)(486)	
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ctg tgt ggt ctg ctg gtt tca ctt tcc ctg tcc att tgc tcc gcg g Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala A 20 25 30	gat 97 Asp
gcc ctg ctc cac agc ctc atg ctg ctg cag ctg tcc ttc tgc aca g Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr A 35 40 45	
ctt gaa atc tcc ctt ttc ttc tgt gaa gtc gtt cag gtc gtc aag c Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys I 50 55 60	etc 193 Jeu
gcg tgc tcc gat acc ctc gtc aac aac ctt ctg atc tat ttt gca g Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala A 65 70 75	gct 241 Ala 30
tgc acc ttg ggt ggc att cct ctg tct ggc atc att ttt tct tac a Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr T 85 90 95	act 289 Thr
caa ata gcc acc tcc att ttg aaa atg ccg tca tcg ggc aga aag t Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys T 100 105 110	at 337 Tyr
aaa gcc ttt tcc acc tgt ggg tct cac ctg tca gtt gtt tcc ctg t Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu F 115 120 125	
tat ggg aca ggt ttg ggg gtg tac atc agt tct gca gtt tct gac t Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp S 130 135 140	
tca agg agg act gcg gtg gct tca gtg atg tac act gtg gtc act c	ccc 481

Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 150 155 160 tgt tg 486 Cys <210> 274 <211> 161 <212> PRT <213> Eulemur rubriventer <220> <221> misc_feature <222> (1)..(486) <223> Taxon = 34829; gene = ERU167; Accession DDBJ/EMBL/GenBank = AF179790 <400> 274 Val Ala Ile Cys His Pro Leu Arg Tyr Thr Asp Ile Met Thr Pro Arg Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp 20 25 Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp 40 Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr 85 90 Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr 100 105 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120 125 Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser 135 Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 155 160 145 150 Cys <210> 275 <211> 487

<212> DNA <213> Eulemur rubriventer													
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<220> <221> CDS <222> (2)(487) <223> Product = olfactory receptor													
<pre><400> 275 t gtg gcc atc tgt cac cct ctg aca tac aca gac atc atg act cct cgt Val Ala Ile Cys His Pro Leu Thr Tyr Thr Asp Ile Met Thr Pro Arg 1 5 10 15</pre>													
ctg tgt ggt ctg ctg gtt tca ctt tcc ctg tcc att tgc tcc gcg gat Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp 20 25 30	97												
gcc ctg ctc cac agc ctc atg ctg ctg cag ctg tcc ttc tgc aca gac Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp 35 40 45	145												
ctt gaa atc tcc ctt ttc ttc tgt gaa gtc gtt cag gtc gtc aag ctc Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu 50 55 60	193												
gcg tgc tcc gat acc ctc gtc aac aac ctt ctg atc tat ttt gca gct Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala 65 70 75 80	241												
tgc acc ttg ggt ggc att cct ctg tct ggc atc att ttt tct tac act Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr 85 90 95	289												
caa ata gcc acc tcc att ttg aaa atg ccg tca tcg ggc aga aag tat Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr 100 105 110	337												
aaa gcc ttt tcc gcc tgt ggg tct cac ctg tca gtt gtt tcc ctg ttc Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	385												
tat ggg aca ggt ttg ggg gtg tac atc agt tct gca gtt tct gac tct Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser 130 140	433												
tca agg agg act gcg gtg gct tca gtg atg tac act gtg gtc act ccc Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155	481												
gtg ttg Val Leu	487												
<210> 276 <211> 162 <212> PRT <213> Eulemur rubriventer													
<220> <221> misc_feature													

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<222> (1)..(487)
<223> Taxon = 34829; gene = ERU168; Accession DDBJ/EMBL/GenBank = AF179791
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Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp
                                25
Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp
Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu
    50
Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala
Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr
Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr
                                105
Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
                            120
Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser
    130
Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
                                        155
Val Leu
<210> 277
 <211> 486
 <212> DNA
 <213> Macaca sylvanus
 <220>
 <221> misc_feature
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 <223> Taxon = 9546; gene = MSY172; Accession DDBJ/EMBL/GenBank = AF179792
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 <221> CDS
       (1)..(486)
 <222>
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cct gcc atc tgc cag cca ctc agg tac cgc gtg ctc atg aac cac cgg

<223> Product = olfactory receptor

<400> 277

Pro A	la	Ile	Cys	Gln 5	Pro	Leu	Arg	Tyr	Arg 10	Val	Leu	Met	Asn	His 15	Arg	
ctc t Leu C	gt Cys	gtg Val	ctg Leu 20	ctg Leu	gtg Val	gga Gly	gct Ala	gcc Ala 25	tgg Trp	gtc Val	ctc Leu	tgc Cys	ctc Leu 30	ctc Leu	aag Lys	96
tcg g Ser V	gtg /al	act Thr 35	gag Glu	aca Thr	gtc Val	att Ile	gcc Ala 40	atg Met	agg Arg	ctg Leu	ccc Pro	ttc Phe 45	tgt Cys	ggc Gly	cac His	144
cac g His V	gtg /al 50	gtc Val	agt Ser	cac His	ttc Phe	acc Thr 55	tgc Cys	gag Glu	atc Ile	ctg Leu	gcg Ala 60	gtg Val	ctg Leu	aag Lys	ctg Leu	192
acg t Thr 0	cgc Cys	ggt Gly	aac Asn	aca Thr	tcg Ser 70	gtc Val	agc Ser	gag Glu	gtc Val	ttc Phe 75	ctg Leu	ctg Leu	gtg Val	ggc Gly	tcc Ser 80	240
atc o	ctg Leu	ctg Leu	ctg Leu	cct Pro 85	gtg Val	ccc Pro	ctg Leu	gca Ala	ttc Phe 90	att Ile	tgc Cys	ctg Leu	tcc Ser	tac Tyr 95	ttg Leu	288
ctc a Leu I	atc Ile	ctg Leu	gcc Ala 100	Thr	atc Ile	ctg Leu	agg Arg	gtg Val 105	Pro	tca Ser	gct Ala	gct Ala	999 Gly 110	tgc Cys	cgc Arg	336
aaa (Lys	gcc Ala	ttc Phe 115	Ser	acc Thr	tgc Cys	tca Ser	gca Ala 120	cac	ctg Leu	gct Ala	gtg Val	gtg Val 125	ctg Leu	ctt Leu	ttc Phe	384
tac Tyr	agc Ser 130	acc Thr	atc Ile	ato : Ile	tto Phe	acg Thr 135	Tyr	ato Met	aag Lys	ccc Pro	aag Lys 140	ser	aag Lys	gaa Glu	gcc Ala	432
cac His 145	atc Ile	tct Ser	gat Asp	gag Glu	gto Val	. Phe	aca Thr	gto Val	c ctc L Leu	tac Tyr 155	. AT	atg Met	gto Val	aca Thr	ccc Pro 160	480
atg Met	_															486
<210 <211 <212 <213	l > 2 >	278 162 PRT Maca	aca :	sylv	anus											
<220 <221 <222 <223	1 > 2 >	(1)	-/1	atur 86) 954		ene	= MS	Y172	; Ac	cess:	ion	DDBJ	/EMB	L/Ge:	nBank	= AF179792
<400	0>	278														
Pro 1	Ala	a Il	е Су	s Gl 5	n Pr	o Le	u Ar	g Ty	r Ar 10	g Va	l Le	u Me	t As	n Hi 15	s Arg	
Leu	Су	s Va	l Le 20		u Va	1 G1	y Al	a Al 25	a Tr	p Va	l Le	u Cy	s Le 30	u Le	u Lys	
Ser	· Va	1 Th 35		u Th	ır Və	.1 I1	e Al 40		et Ar	g Le	u Pr	o Ph 45	.е Су	s Gl	y His	

His Val Val Ser His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu 55 50

Thr Cys Gly Asn Thr Ser Val Ser Glu Val Phe Leu Leu Val Gly Ser 70

Ile Leu Leu Pro Val Pro Leu Ala Phe Ile Cys Leu Ser Tyr Leu

Leu Ile Leu Ala Thr Ile Leu Arg Val Pro Ser Ala Ala Gly Cys Arg 105

Lys Ala Phe Ser Thr Cys Ser Ala His Leu Ala Val Val Leu Leu Phe 120

Tyr Ser Thr Ile Ile Phe Thr Tyr Met Lys Pro Lys Ser Lys Glu Ala 135 130

His Ile Ser Asp Glu Val Phe Thr Val Leu Tyr Ala Met Val Thr Pro 155 150 145

Met Leu

<210> 279

489 <211> <212> DNA

<213> Macaca sylvanus

<220>

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(1)..(489) <222>

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<210> 280

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<211> 481
<212> DNA
<213> Macaca sylvanus
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<221> misc_feature
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<220>
<221> CDS
<222> (2)..(481)
<223> product = olfactory receptor
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                                                                       49
  Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat
                                                                       97
Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
                                25
gga ggg atc cag act ttg ttc ata gcc cac tta cca ttc tgt ggc cct
                                                                      145
Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro
aat gtc atc gac cac ttt atg tgt gat tta gta cct ctt cta gag ctg
                                                                      193
Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
    50
gcc tgc aca gac act cac acc ttg ggg cct ctg ata gct gcc aac agt
                                                                      241
Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
gga tca ttg tgt ttc ctc att ttt tcc atg ctg gtt gct tcc tat gtc
                                                                      289
Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
                                     90
atc atc ctg tgc tcc cta agg act cat atc tct gaa ggg cgt cac aaa
                                                                      337
Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
                                 105
gtt ctg tct agt tgt acc tct cat atc ttt gtt gtc atc tta ttc ttt
                                                                      385
 Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
                             120
         115
 gtc cct tgt tca tac ctg tat cta aga cct cta acc tcc ttc ttc ccc
                                                                       433
 Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro
     130
 act gac aaa gct gtg act gtg ttt tgc acc cta ttt aca cct atg ttg
                                                                       481
 Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
                                         155
                     150
 145
 <210> 281
 <211>
        160
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 <223> Taxon = 9546; gene = MSY174; Accession DDBJ/EMBL/GenBank = AF179794
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<400> 281

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Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His

Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro

Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu

Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser

Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val 95

Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys 105 100

Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe 115

Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro

Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu 150

<210> 282

<211> 402

<212> DNA

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(402)

<223> Taxon = 9546; gene = MSY175; pseudogene; Accession DDBJ/EMBL/GenBank = AF179795*

<400> 282

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<210> 283
<211> 487
<212> DNA
      Macaca sylvanus
<220>
<221> misc_feature
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       Taxon = 9546; gene = MSY176; Accession DDBJ/EMBL/GenBank = AF179796
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<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 283
c gtg gct att tgc aac cct ctg ctc tac gca tta gtg gtg tct cca aag
  Val Ala Ile Cys Asn Pro Leu Leu Tyr Ala Leu Val Val Ser Pro Lys
gta tgt cgt ctg ctg gtg tcc ctc aca tac ctt cag agt ctt atc aca
                                                                        97
Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile Thr
gcc ctt act gtc tct tcc tgt gtg ttc tct gtg tca tac tgt tct tcc
                                                                       145
Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser Ser
                             40
                                                                       193
aac atc atc aac cat ttt tac tgt gac gat gtc cct ttg cta gca ttg
Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala Leu
                         55
 tcg tgt tct gat acc tac att cca gaa aca gca gtg ttt atc ttt tca
                                                                       241
Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe Ser
 65
 ggg acc aat ttg ttt ttc tcc atg acc gtt gtt ctg ata tcc tac ttc
                                                                       289
 Gly Thr Asn Leu Phe Phe Ser Met Thr Val Val Leu Ile Ser Tyr Phe
 aac att gtt att acc att ttg agg ata cgt tcc tca gaa gga cga caa
                                                                       337
 Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Gln
                                 105
                                                                        385
 aaa gcc ttt tcc acg tgt gct tct cac atg ata gct gtg gtt gtg ttc
 Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Phe
                             120
 tat ggg act ctc ctt ttc atg tat ttg caa cca agg agt aat cac tca
                                                                        433
 Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His Ser
     130
                          135
 tta gat act gac aaa atg gcc tcg gtc ttc tac acc ctg atc ata cct
                                                                        481
 Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Ile Ile Pro
                                                              160
                     1.50
 145
                                                                        487
 atg ttg
 Met Leu
```

<220>

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<211> 162
<212> PRT
<213> Macaca sylvanus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9546; gene = MSY176; Accession DDBJ/EMBL/GenBank = AF179796
<400> 284
Val Ala Ile Cys Asn Pro Leu Leu Tyr Ala Leu Val Val Ser Pro Lys
Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile Thr
                                 25
            20
Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser Ser
Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala Leu
Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe Ser
Gly Thr Asn Leu Phe Phe Ser Met Thr Val Val Leu Ile Ser Tyr Phe
Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Gln
             100
Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Phe
         115
 Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His Ser
                         135
 Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Ile Ile Pro
                    150
 Met Leu
 <210> 285
 <211> 487
<212> DNA
 <213> Macaca sylvanus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY177; Accession DDBJ/EMBL/GenBank = AF179797
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<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
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  Val Ala Ile Cys His Pro Leu His Tyr Ala Ile Ile Met Gly Gln Ser
                  5
                                      10
                                                                       97
cag tgt gtc acg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
                                25
gct ctt ttg cac act ctc ctc ctg gcc tgg ctt tcc ttc tgt gct gat
                                                                      145
Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg
                                                                       193
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
                        55
tee tge tea gae ace tee ete aat eag tta gea ate ttt aca gea gga
                                                                       241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
                    70
                                                                       289
ttg aca gcc att atg ctt cca ttc ctg tgt atc ctg gtt tct tat ggt
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                                     90
                                                                       337
cac act gca gtc acc atc ctc cag att ccc tct act aat ggc ata tgc
His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys
                                 105
            100
aaa gcc ttg tcc act tgt gga tcc cac ctc tca gca gtg act ctc tat
                                                                       385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr
                             120
tat ggg acc att att ggt ctc tat ttt ctt ccc cca tcc agc aac act
                                                                       433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
                         135
 aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc
                                                                       481
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                                         155
                     150
                                                                       487
 atg ttg
Met Leu
 <210> 286
 <211> 162
 <212>
       PRT
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       misc_feature
 <222>
        (1)..(487)
       Taxon = 9546; gene = MSY177; Accession DDBJ/EMBL/GenBank = AF179797
 <223>
 <400> 286
 Val Ala Ile Cys His Pro Leu His Tyr Ala Ile Ile Met Gly Gln Ser
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Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 25

Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 55

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly

His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys 105 100

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr 115 120

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 135 130

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 155

Met Leu

<210> 287

<211> 487

<212> DNA <213> Macaca sylvanus

<220>

<221> misc_feature

(1)..(487) <222>

<223> Taxon = 9546; gene = MSY178; Accession DDBJ/EMBL/GenBank = AF179798

<220>

<221> CDS

<222> (2)..(487)

<223> product = olfactory receptor

<400> 287

t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg 49 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met

ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gta ctg acc acc ttc cat 97 Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 25

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac 145 Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp

40 35 aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg 193 Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu gcc tgc tct gac act caa gtt aat gaa ttg gcg ata ttt atc acg gga 241 Ala Cys Ser Asp Thr Gln Val Asn Glu Leu Ala Ile Phe Ile Thr Gly ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca 289 Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 85 cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc 337 Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 105 100 aag gcc ttc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 385 125 120 115 tat ggg acc gtt att ggt ctc tac ttc tgc cca tca gct aat agt tct 433 Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser act cta aag gag act gtc atg gct atg atg tac act gtg gtg acc ccc 481 Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 150 487 atg ctg Met Leu <210> 288 <211> 162 <212> PRT <213> Macaca sylvanus <220> <221> misc_feature (1)..(487) <222> Taxon = 9546; gene = MSY178; Accession DDBJ/EMBL/GenBank = AF179798

Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 50 60

Ala Cys Ser Asp Thr Gln Val Asn Glu Leu Ala Ile Phe Ile Thr Gly 65 70 75 80

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Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                                    90
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
                    150
                                        155
Met Leu
<210> 289
<211>
       484
<212> DNA
<213> Macaca sylvanus
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<222> (1)..(484)
<223> Taxon = 9546; gene = MSY179; Accession DDBJ/EMBL/GenBank = AF179799
<220>
<221> CDS
 <222> (2)..(484)
 <223> Product = olfactory receptor
 <400> 289
 a tgt gcc atc tgc tgc ccc ctc cac tac acc aca gcc atg agc cct aag
                                                                       49
  Cys Ala Ile Cys Cys Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys
                                       10
                                                                       97
 ctc tgt atc tta ctc ctt tcc ttg tgt tgg gtc tta tct gtg ctc tat
 Leu Cys Ile Leu Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr
             20
                                                                      145
 ggc ctc ata cac acc ttc ctc atg acc acg gtg acc ttc tgt ggg tca
 Gly Leu Ile His Thr Phe Leu Met Thr Thr Val Thr Phe Cys Gly Ser
                                                                      193
 cga aaa atc cac tac atc ttc tgt gag atg tat gta ttg ctg agg ctg
 Arg Lys Ile His Tyr Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Leu
                                             60
 gca tgt tcc gac act cag att aat cac aca gtg ctg att gcc aca ggc
                                                                       241
 Ala Cys Ser Asp Thr Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly
                     70
                                                                       289
 tgc ttt atc ttc ctc att ccc ttt gga ttc atg atc att tcc tat gtg
 Cys Phe Ile Phe Leu Ile Pro Phe Gly Phe Met Ile Ile Ser Tyr Val
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ttg att gtc aga gcc atc ctc aga ata ccc tca gtc tct aag aaa tac

85

Leu Ile Val	Arg Ala 100	Ile Leu	Arg Ile 105	Pro Ser	Val Ser	Lys Ly 110	s Tyr			
aaa gcc ttc Lys Ala Phe 115	tcc act Ser Thr	tgt gcc Cys Ala	tcc cat Ser His 120	ttg ggt Leu Gly	gta gtc Val Val 125	tcc ct Ser Le	c ttc u Phe	385		
tat ggg aca Tyr Gly Thr 130	ctt tgt Leu Cys	atg gta Met Val 135	tac ctg Tyr Leu	aag ccc Lys Pro	c ctc cat Leu His 140	acc ta Thr Ty	c tct r Ser	433		
gtg aag gac Val Lys Asp 145	tca gta Ser Val	gcc aca Ala Thr 150	gtg atg Val Met	tat gcg Tyr Ala 155	a Val Val	aca cc Thr Pr	c atg o Met 160	481		
atg Met								484		
<210> 290 <211> 161 <212> PRT <213> Maca	ca sylva	nus								
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<400> 290										
Cys Ala Ile 1	e Cys Cys 5	Pro Leu	His Tyr	Thr Th	r Ala Met	Ser Pi	co Lys			
Leu Cys Ile	e Leu Leu 20	. Leu Ser	Leu Cys 25	s Trp Va	l Leu Se	r Val Le 30	eu Tyr			
Gly Leu Ile 35	e His Thr	Phe Leu	Met Th	r Thr Va	l Thr Ph 45	e Cys G	ly Ser			
Arg Lys Ile 50	e His Tyr	Tle Phe	e Cys Gl	u Met Ty	r Val Le 60	u Leu A	rg Leu			
Ala Cys Se: 65	r Asp Thr	Gln Ile 70	e Asn Hi	s Thr Va 75	al Leu Il S	e Ala T	hr Gly 80			
Cys Phe Il	e Phe Lei 85	ı Ile Pro	o Phe Gl	y Phe Me 90	et Ile Il	e Ser T 9	yr Val 5			
Leu Ile Va	l Arg Ala 100	a Ile Lev	ı Arg Il 10		er Val Se	r Lys I 110	ys Tyr			
Lys Ala Ph 11		r Cys Ala	a Ser Hi 120	s Leu G	ly Val Va 12	ıl Ser I 25	eu Phe			
Tyr Gly Th	r Leu Cy	s Met Vai		eu Lys P:	ro Leu Hi 140	s Thr 1	Cyr Ser			

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Met
<210> 291
      487
<211>
<212>
      DNA
<213> Macaca sylvanus
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= AF179800
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tgctgccata tgtcaccctc tccattacac tgccatcatg agggaagagc tctgtgtctt
                                                                       60
cttagtggct gtatcttgaa ttctgtcttg tgccagctcc ctctctcaca cccttctcct
                                                                      120
gacceagetg tetttetgtg etgegaacae catececcae atettetgtg acettgetge
                                                                      180
cctgctcaag ctgtcctggt cagatatctt cctcaatgag ctggtcatgt tcacagtagg
                                                                      240
ggtggtggtc attaccctgc cattcatgtg tatcctggta tcatatggct acactggggc
                                                                      300
caccatcctg agggtccctt caaccaaagg gatccacaaa gcattgtcca catgtgcctc
                                                                      360
ccatctctct gtggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac
                                                                      420
tgtaagcagt tctattgaca aggatgttac tgtggctctc atgtacatcg tggtcacacc
                                                                      480
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 cgtgttg
 <210> 292
 <211>
       487
       DNA
 <212>
 <213> Macaca sylvanus
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 <223> Taxon = 9546; gene = MSY181; pseudogene; Accession DDBJ/EMBL/GenBank
 = AF179801
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                                                                        60
 cttagtggct gtatcttgaa ttctgtcttg tgccagctcc ctctctcaca cccttctcct
                                                                       120
 gacccagctg tetttetgtg etgegaacae cateccecae atettetgtg acettgetge
                                                                       180
 cctgctcaag ctgtcctggt cagatatctc cctcaatgag ctggtcatgt tcacagtagg
                                                                       240
 ggtggtggtc attaccetge catteatgtg tateetggta teatatgget acaetgggge
                                                                       300
 caccatectg agggtccctt caaccaaagg gatccacaaa gcattgtcca catgtgcctc
                                                                       360
 ccatctctct gtggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac
                                                                       420
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Val Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr Pro Met

150

145

tgtaa	gcag	gt to	ctatt	gac	a agg	gatgi	ttac	tgt	ggcto	ctc a	atgt	acato	g to	ggtca	acacc	480	
cgtgt	tg															487	
<210><211><212><213>	48 DN	37 IA	a sy:	lvan	us												
<220; <221; <222; <223;	> m:	1)	feat: (487 = 9:)	gen	e = 1	MSY1	82;	Acce	ssio	n DD	BJ/E	MBL/	GenB:	ank =	AF17980	2
<220> <221> CDS <222> (2)(487) <223> Product = olfactory receptor																	
<400: t gtg Va: 1	7 00	93 c at a Il	c tg e Cy	t aa s Ly 5	a cc s Pr	c ct o Le	t ca eu Hi	t ta s Ty	t at r Me 10	t Va	c at l Il	c at e Me	g aa t As	c aa n As 15	c agg n Arg	49	
gtg Val	tgt Cys	acc Thr	tta Leu 20	tta Leu	gtc Val	ctc Leu	tgc Cys	agt Ser 25	tgg Trp	gtg Val	gct Ala	ggc Gly	ttg Leu 30	atg Met	atc Ile	97	
att Ile	gtt Val	cca Pro 35	cca Pro	ctg Leu	agc Ser	tta Leu	ggc Gly 40	ctc Leu	cag Gln	ctc Leu	gaa Glu	ttc Phe 45	tgt Cys	ggc Gly	tcc Ser	145	
Asn	gcc Ala 50	att Ile	gat Asp	cat His	ttt Phe	agc Ser 55	tgt Cys	gat Asp	gca Ala	ggt Gly	cct Pro 60	ctc Leu	cta Leu	aag Lys	atc Ile	193	
tca Ser 65	tgc Cys	tca Ser	gac Asp	aca Thr	tgg Trp 70	gta Val	ata Ile	gaa Glu	cag Gln	ata Ile 75	gtt Val	ata Ile	ctt Leu	atg Met	gct Ala 80	241	
gta Val	ttt Phe	gca Ala	ctc Leu	att Ile 85	atc Ile	acc Thr	cta Leu	gtt Val	tgt Cys 90	gtg Val	att Ile	ctg Leu	tcc Ser	tac Tyr 95	ttg Leu	289	
tac Tyr	ata Ile	gtc Val	aga Arg 100	aca Thr	att Ile	ctg Leu	agg Arg	ttc Phe 105	cct Pro	tct Ser	gtt Val	cag Gln	caa Gln 110	agg Arg	aaa Lys	337	
aag Lys	gcc Ala	ttt Phe 115	Ser	acc Thr	tgt Cys	tca Ser	tcc Ser 120	His	atg Met	att Ile	gtg Val	gtt Val 125	tcc Ser	att Ile	gcc Ala	385	
tat Tyr	gga Gly 130	agc Ser	tgc Cys	atc Ile	ttc Phe	gtc Val 135	Tyr	atc Ile	aag Lys	ccc Pro	tct Ser 140	A⊥a	aaa Lys	gat Asp	gaa Glu	433	
gtg Val 145	gcc Ala	ata Ile	aat Asn	aaa Lys	gga Gly 150	Val	tca Ser	gtt Val	. ctt . Leu	act Thr 155	Thr	tct Ser	gtt Val	gca Ala	ccc Pro 160	481	
_	ttg Leu															487	

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<210> 294
<211> 162
<212> PRT
<213> Macaca sylvanus
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<222> (1)..(487)
<223> Taxon = 9546; gene = MSY182; Accession DDBJ/EMBL/GenBank = AF179802
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Val Ala Ile Cys Lys Pro Leu His Tyr Met Val Ile Met Asn Asn Arg
Val Cys Thr Leu Leu Val Leu Cys Ser Trp Val Ala Gly Leu Met Ile
                                 25
Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Gly Ser
Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Ile Val Ile Leu Met Ala
                     70
 Val Phe Ala Leu Ile Ile Thr Leu Val Cys Val Ile Leu Ser Tyr Leu
                                     90
                 85
 Tyr Ile Val Arg Thr Ile Leu Arg Phe Pro Ser Val Gln Gln Arg Lys
                                 105
 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
                              120
 Tyr Gly Ser Cys Ile Phe Val Tyr Ile Lys Pro Ser Ala Lys Asp Glu
 Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
                                          155
 Leu Leu
 <210> 295
 <211> 487
 <212> DNA
 <213> Callithrix jacchus
 <220>
  <221> misc_feature
        (1)..(487)
  <222>
  <223> Taxon = 9483; gene = CJA169; Accession DDBJ/EMBL/GenBank = AF179803
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<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
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  Val Ala Ile Cys Arg Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
                                      10
                                                                       97
gtc tgt gcc cta atc ctt gca ttg tgc tgg gtc ctc acc aat gtt gtt
Val Cys Ala Leu Ile Leu Ala Leu Cys Trp Val Leu Thr Asn Val Val
            20
gcc ctg act cac aca ctc ctc atg gct cga ctg tcc ttc tgt gtg act
                                                                      145
Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
ggg gaa ata gct cac ttt ttc tgt gac atc act cct gtc ctg aag cta
                                                                      193
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
                        55
                                                                      241
tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
                     70
ggc aca gta ctc att gtc ccc ttt ata tgc att gtc acc tcc tac atc
                                                                       289
Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile
                85
                                                                       337
cac att gtg cct gct atc ctg agg gtc cga acc tgt ggt ggg gcg ggc
His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly
aag gcc ttt tcc acc tgc agt tcc cac ctc tgc att gtt tgt ata ttc
                                                                       385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe
                             120
tat ggg ace ctc ttc agt gcc tac ctg tgt cct ccc tct att gcc tct
                                                                       433
Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
                         135
gaa gag aag gac att gca gca gct gca ctg tat acc ata gtg act ccc
                                                                       481
Glu Glu Lys Asp Ile Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro
                                                              160
                     150
145
                                                                       487
 atg ttg
Met Leu
 <210> 296
 <211> 162
 <212> PRT
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       (1)..(487)
 <223> Taxon = 9483; gene = CJA169; Accession DDBJ/EMBL/GenBank = AF179803
 Val Ala Ile Cys Arg Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
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- Val Cys Ala Leu Ile Leu Ala Leu Cys Trp Val Leu Thr Asn Val Val 2.5
- Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
- Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
- Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
- Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile
- His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly 100
- Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe 120
- Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser 130 135
- Glu Glu Lys Asp Ile Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro 155

Met Leu

- <210> 297
- <211> 486
- <212> DNA
- <213> Callithrix jacchus
- <220>
- <221> misc_feature
- <222> (1)..(486)
- <223> Taxon = 9483; gene = CJA170; Accession DDBJ/EMBL/GenBank = AF179804
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- <222> (1)..(486) <223> Product = olfactory receptor
- <400> 297
- gtg gcc atc tgt cac cca ctg cac tac aca gtc acc att aac ccc aga 48 Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
- ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat 96 Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn 3.0 20

tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca ga Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr As 35 40 45	ic 144 sp
ttg gaa atc ccc cgc ttt ttc tgc gaa ctt aat cag gtc atc cac ct Leu Glu Ile Pro Arg Phe Phe Cys Glu Leu Asn Gln Val Ile His Le 50 55 60	eu 192
gcc tgt tct gac act ttt ctt aat gat gtg gtg atg tat ttg gcc gc Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Al 65 70 75	La
gtg ctg ctg ggg ggt ggt ccc ctt gca ggg att ctt tac tct tac tc Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Se 85 90 95	ct 288 er
aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag ta Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys T 100 105 110	ac 336 yr
aag gca ttt tcc acc tgt gta tct cac atc tta att gtc tcc tta t Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu P 115 120 125	tt 384 he
tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gca act ggc a Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly A 130 135	ac 432 sn
tca cat tca aga gct gca gcc tcg gtg atg tac act gtg gtc acc c Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr P 145 150 155	ecc 480 Pro .60
atg ctg Met Leu	486
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Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro 1 10 15	Arg
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu 20 25 30	Asn
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr 35 40 45	Asp
Leu Glu Ile Pro Arg Phe Phe Cys Glu Leu Asn Gln Val Ile His 50 55 60	Leu

75

Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser 90

70

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr 100

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe 120

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 140 130 135

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro 155 150

Met Leu

<210> 299 <211> 487 <212> DNA <213> Callithrix jacchus <220> <221> misc feature

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<223> Product = olfactory receptor

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gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gct ttg ggg 97 Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ala Leu Gly

gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt gca gaa 145 Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu

ace ctt gtc aat cac tac atg tgt gac atc ctt ccc ctc ctt gag ctc 193 Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu 55

241 tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val 70

acc att ggc att ggg gtg ccc att gtc acc att ttt atc tct tat ggt 289 Thr Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 90 85

ttt att ctt tcc agc att ctc cac att agt tct gct gag ggc agg tct Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser 100 105 110	37
aaa gcc ttc agt acc tgc agc tcc cac ata gtt gtg gta ttg ctt ttc Lys Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Leu Leu Phe 115 120 125	85
ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 130 135 140	33
ctg gac cag ggg aaa gtg tcc tcc att ttt tat act gcg gtg gtg ccc Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 145 150 160	81
atg ttt Met Phe	87
<210> 300 <211> 162 <212> PRT <213> Callithrix jacchus	
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<400> 300	
Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln 1 5 15	
Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ala Leu Gly 20 25 30	
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu 35 40 45	
Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu 50 55 60	
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val 65 70 75 80	
Thr Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 85 90 95	
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser 100 105 110	
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Val Leu Leu Phe 115 120 125	

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 145 150 155 160

Met Phe

<210: <211: <212: <213:	> 48 > DI	01 37 NA alli	thri:	x ja	cchu	s											
<220: <221: <222: <223	> m:	1) —	feat (487 = 9	}	gen	e = (CJA1	96;	Acce	ssio	n DD:	BJ/E	MBL/	GenB	ank =	AF17	9806
<220 <221 <222 <223	> C		(487 .ct =		acto	ry r	ecep	tor									
<400 c tt Le 1	מ מכ	01 c at a Il	.c tg .e Cy	c ca s Hi 5	c cc s Pr	g ct o Le	g ca u Hi	c ta s Ty	c to r Se 10	r Se	c aa r Ly	g at s Me	g ag t Se	c ct r Le 15	g tgc u Cys		49
agc Ser	tgc Cys	acc Thr	cta Leu 20	atg Met	ttg Leu	ggc Gly	tgc Cys	tta Leu 25	tgg Trp	acc Thr	act Thr	gcc Ala	agc Ser 30	ctc Leu	cat His		97
gcc Ala	ctt Leu	ctg Leu 35	cac His	acc Thr	ctt Leu	ctc Leu	ttg Leu 40	gcc Ala	cgg Arg	ctg Leu	gac Asp	ttc Phe 45	tgt Cys	gcc Ala	agc Ser	-	L45
aat Asn	gtt Val 50	atc Ile	ccc Pro	tac Tyr	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctc Leu	gtt Val	ccc Pro 60	ctg Leu	ctc Leu	cag Gln	ctc Leu	:	193
tcc Ser 65	tgt Cys	tct Ser	gac Asp	acc Thr	cga Arg 70	ctc Leu	aac Asn	cag Gln	ctc Leu	atg Met 75	att Ile	gtg Val	ctg Leu	gtg Val	80 GJA āāā	:	241
ggc	ctg Leu	atc Ile	atc Ile	ctc Leu 85	ctg Leu	ccc Pro	ttc Phe	ctt Leu	ggc Gly 90	att Ile	ctc Leu	ggt Gly	tcc Ser	tac Tyr 95	aca Thr		289
tgc Cys	att Ile	gca Ala	gct Ala 100	gca Ala	gtg Val	ctc Leu	aga Arg	gtc Val 105	ccc Pro	tct Ser	gcc Ala	agg Arg	ggt Gly 110	acg Thr	tgg Trp		337
aag Lys	gcc Ala	ttt Phe 115	Ser	acc Thr	tgt Cys	ggc	tcc Ser 120	cac His	ctg Leu	acc Thr	atg Met	gtc Val 125	atc Ile	ctc Leu	ttc Phe		385
tat Tyr	ggc Gly 130	Thr	atc Ile	tca Ser	gly aaa	gtc Val 135	tac Tyr	ctg Leu	agg Arg	ccc	tca Ser 140	Ser	tcc Ser	cac His	tcc Ser		433
aca Thr	gac Asp	aag Lys	gac Asp	tca Ser	cta Leu	gcc Ala	tca Ser	gtg Val	atg Met	tac Tyr	atg Met	gta Val	gtg Val	acc Thr	ccc Pro		481

145 150 155 160 atg ctg 487 Met Leu <210> 302 <211> 162 <212> PRT <213> Callithrix jacchus <220> <221> misc_feature <222> (1)..(487) <223> Taxon = 9483; gene = CJA196; Accession DDBJ/EMBL/GenBank = AF179806 <400> 302 Leu Ala Ile Cys His Pro Leu His Tyr Ser Ser Lys Met Ser Leu Cys Ser Cys Thr Leu Met Leu Gly Cys Leu Trp Thr Thr Ala Ser Leu His Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Asp Phe Cys Ala Ser Asn Val Ile Pro Tyr Phe Phe Cys Asp Leu Val Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Asn Gln Leu Met Ile Val Leu Val Gly 70

Gly Leu Ile Ile Leu Leu Pro Phe Leu Gly Ile Leu Gly Ser Tyr Thr 85 90 95

Cys Ile Ala Ala Ala Val Leu Arg Val Pro Ser Ala Arg Gly Thr Trp \$100\$ \$105\$

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Met Val Ile Leu Phe 115 120 125

Tyr Gly Thr Ile Ser Gly Val Tyr Leu Arg Pro Ser Ser His Ser 130 135 140

Thr Asp Lys Asp Ser Leu Ala Ser Val Met Tyr Met Val Val Thr Pro 145 150 160

Met Leu

<210> 303 <211> 487 <212> DNA

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<213> Callithrix jacchus
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<222>
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      Taxon = 9483; gene = CJA197; Accession DDBJ/EMBL/GenBank = AF179807
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<222> (2)..(487)
<223> Product = olfactory receptor
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  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
                                          10
ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat
                                                                             97
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
                                   25
tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac
                                                                            145
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
                               40
ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc atc cac ctt
                                                                            193
Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
    50
gcc tgt tct gac act ttt ctt aat gat gtg gtg atg tat ttg gcc gct
Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
                                                                            241
                       70
 gtg ctg ctg ggg ggt ggt ccc ctt gca ggg att ctt tac tct tac tct
                                                                            289
 Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser
                  85
 aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac
Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
                                                                             337
                                   105
              100
 aag gca ttt tcc acc tgt gta tct cac atc tta att gtc tcc tta ttt
                                                                             385
 Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe
                                120
          115
 tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gca act ggc aac
                                                                             433
 Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
     130
 tca cat tca aga gct gca gcc tcg gtg atg tac act gtg gtc acc ccc
                                                                             481
 Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro
                                             155
                                                                             487
 atg ctg
 Met Leu
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Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu 55

Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala

Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser 90

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 135

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro 155

Met Leu

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<210> 305
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<213> Callithrix jacchus

<220>

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<223> Taxon = 9483; gene = CJA198; Accession DDBJ/EMBL/GenBank = AF179808

<220>

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<222> (2)..(487)
<223> Product = olfactory receptor

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<211> 487

<212> DNA

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tct Ser	aca Thr	att Ile 35	cac His	acc Thr	agc Ser	tct Ser	atg Met 40	ttg Leu	aga Arg	ctc Leu	ttt Phe	ctg Leu 45	tgc Cys	aaa Lys	act Thr		145	
aat Asn	gtg Val 50	att Ile	aac Asn	cat His	tat Tyr	ttt Phe 55	tgt Cys	gat Asp	ctc Leu	ttc Phe	cct Pro 60	ctc Leu	ttg Leu	gaa Glu	ctc Leu		193	
tcc Ser 65	tgc Cys	tcc Ser	agt Ser	acc Thr	tac Tyr 70	atc Ile	aat Asn	gaa Glu	tta Leu	cta Leu 75	gtt Val	ctg Leu	gtc Val	ttg Leu	agt Ser 80		241	
gca Ala	ttg Leu	aat Asn	atc Ile	ctg Leu 85	acg Thr	cct Pro	gcc Ala	tta Leu	act Thr 90	atc Ile	ctg Leu	gcc Ala	tct Ser	tat Tyr 95	atc Ile		289	
ttc Phe	acc Thr	att Ile	gcc Ala 100	agt Ser	atc Ile	ctc Leu	cac His	att Ile 105	cgc Arg	tcc Ser	act Thr	gag Glu	ggc Gly 110	agg Arg	tcc Ser		337	
aaa Lys	gcc Ala	ttc Phe 115	Ser	act Thr	tgc Cys	agc Ser	tcc Ser 120	cac His	atc Ile	tca Ser	gct Ala	gtt Val 125	Ата	gtc Val	ttc Phe		385	
ttt Phe	gga Gly 130	Ser	gca Ala	gca Ala	ttc Phe	atg Met 135	Tyr	ctg Leu	cag Gln	g cca Pro	tca Ser 140	ser	gtc Val	agt Ser	tcc Ser		433	
atg Met	Asp	cag Gln	gly ggg	ı aaa ′ Lys	gtg Val	Ser	tct Ser	gtg Val	ttt Phe	tac Tyr 155	1111	a act Thr	gtt Val	gtg Val	ccc Pro 160		481	
_	ctg Leu																487	
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< 4	00>	306																
11	e Ala	a Il	е Су	s Se 5	r Pr	o Le	u Le	u Ty	r As 10	n Va	1 I1	e Me	t Se	r Ty 15	r His			
Ph	е Су	s Ph	e Ar 20		u Th	r Va	1 G1	y Va 25	1 Ту	r Il	e Le	u Gl	y I1 30	e Le	u Gly			
Se	r Th	r Il 35		s Th	r Se	r Se	r Me	t Le	u Ar	g Le	u Ph	ıe Le 45	u Cy	s Ly	s Thr			

Asn	Val 50	Ile	Asn	His	Tyr	Phe 55	Cys	Asp	Leu	Phe	Pro 60	Leu	Leu	Glu	Leu		
Ser 65	Cys	Ser	Ser	Thr	Tyr 70	Ile	Asn	Glu	Leu	Leu 75	Val	Leu	Val	Leu	Ser 80		
Ala	Leu	Asn	Ile	Leu 85	Thr	Pro	Ala	Leu	Thr 90	Ile	Leu	Ala	Ser	Tyr 95	Ile		
Phe	Thr	Ile	Ala 100	Ser	Ile	Leu	His	Ile 105	Arg	Ser	Thr	Glu	Gly 110	Arg	Ser		
Lys	Ala	Phe 115		Thr	Cys	Ser	Ser 120		Ile	Ser	Ala	Val 125	Ala	Val	Phe		
Phe	Gly 130		Ala	Ala	Phe	Met 135	Tyr	Leu	Gln	Pro	Ser 140	Ser	. Val	Ser	Ser		
Met 145		Gln	Gly	. Lys	Val	Ser	Ser	Val	. Phe	Tyr 155	Thr	Thi	. Val	. Val	Pro 160		
Met	. Lev	ι															
<2: <2:	10> 11> 12>	307 469 DNA Call	lith:	rix :	jaccl	nus											
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<2 <2	20> 21> 22> 23>	CDS (2) Pro	(4	69) = 0	lfac	tory	rec	epto	r								
	00> gtt Val 1		\neg + σ	tgt Cys	cac His 5	ccc Pro	ctg Leu	cac His	tac Tyr	acc Thr 10	act Thr	gtc Val	atg Met	agt Ser	cgg 9 Arg 0	gga Hy	49
tt L∈	a tg u Cy	rc tg rs Cy	t gt s Va 20	l Le	g gt u Va	t gc 1 Al	t gc a Al	c to a Se	er Tr	g at p Me	g gg t Gl	ja gg .y Gl	ja tt .y Ph 30	1C VC	g cad	3	97
to Se	c ac er Th	c gt ir Va 35	ıl Gl	ng ao .n Th	c at r Il	t ct e Le	c ac u Th	ır I.	c co le Ar	jt at g Le	g co eu Pr	cc tt co Pl 4!	re cy	gt gg /s Gl	gg cca Ly Pro	a O	145
aa As	at ca sn Gl	n Va	g ga al As	ac aa sp As	ac tt sn Pl	t tt ne Ph 55	ie Cž	jt ga 7s Ai	at gt sp Va	t co al Pi	CC CC P1 60	LO V	cc at al II	c aa le Ly	aa ct ys Le	t u	193
g			ct ga	ac a	et tt	t gt	c at	t ga	aa ti	cg ct	cc at	tg g	ta to	ct a	ac ag	t	241

65	Cys	Ala	Asp		Phe 70	Val	Ile	Glu		Leu 75	Met	Val	Ser	Asn	Ser 80			
Gly 333	ttg Leu	atc Ile	tcc Ser	acc Thr 85	agc Ser	tcc Ser	ttt Phe	gtg Val	gtg Val 90	ctg Leu	att Ile	tcc Ser	tcc Ser	tac Tyr 95	acc Thr		2	289
act Thr	atc Ile	cta Leu	gtc Val 100	aag Lys	att Ile	cac His	tcc Ser	aag Lys 105	gag Glu	gga Gly	agg Arg	cga Arg	aag Lys 110	gca Ala	ctc Leu		3	337
tcc Ser	aca Thr	tgt Cys 115	gcc Ala	tct Ser	cac His	ctt Leu	atg Met 120	gtg Val	gta Val	aca Thr	ctt Leu	ttt Phe 125	gga Gly	ccc Pro	tgt Cys		:	385
agt Ser	ttc Phe 130	atc Ile	tat Tyr	cct Pro	cat His	cct Pro 135	ttc Phe	tct Ser	aca Thr	ttt Phe	tct Ser 140	gtg Val	gac Asp	aag Lys	atg Met			433
gtg Val 145	Ser	gta Val	ctc Leu	tac Tyr	aag Lys 150	gtt Val	att Ile	act Thr	cca Pro	atg Met 155	cta Leu							469
<21 <21 <21 <21	1> 2>	308 156 PRT Call	ithr	ix ja	acchi	ıs												
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<40	00>	308																
			e Cys	His 5	Pro													
Val	l Ala	a Il∈	e Cys S Val 20	5		Leu	His	Tyr	Thr	Thr	· Val	. Met	. Sei	15	g Gl	У		
Val 1 Lei	l Ala	a Ile	s Val	5 Leu	Val	Leu Ala	His Ala	Tyr Sei 25	Thr 10	Thr	· Val	. Met	Ser y Phe 30	Arg 15	g Gl	y		
Val 1 Let	l Ala	a Ile s Cys r Val 35	s Val 20	5 Leu Thr	Val	Leu Ala	His Ala Thr 40	Tyr Ser 25	Thr 10 Trp	Thr Met	· Val	. Met y Gl; o Ph 45	y Phe 30	TARGE Value of Galage	g Gl	y s		
Val 1 Let Se	L Ala L Cys Thi Thi 50	a Ile s Cys r Val 35 n Val	s Val 20 l Glr	5 Leu Thr	Val	Leu Ala Leu E Phe 55	His Ala Thr 40	Tyr Ser 25 Ile	Thr 10 Trp e Arg	Thr Met Let	Pro Pro 60	Met Gl: Ph 45	y Phe 30 e Cy:	TATE TO THE TENT OF THE TENT	g Gl L Hi Y Pr	y s co		
Val 1 Let Se As	l Ala ı Cys r Thi n Gli 50	a Ile s Cys r Val 35 n Val	s Val 20 l Glr l Asp	5 Leu Thr Asr	Val	Leu Ala Leu Phe 55	His Ala Thr 40	Tyr 25 Ser 116 Asj	Thr 10 Trp Arg	Met Pro	Val	. Met	y Phe 30 e Cy:	TATE	Gl' Gl' Hi	s o o		
Vall Let Se As Al 65	L Ala L Cys r Thi n Gli 50 a Cy y Le	a Ile s Cys r Val 35 n Val s Al	s Val 20 l Glr l Asp	5 Leu n Thr n Asr n Thr 85	Val	Leu Ala Leu Phe 55	His Ala Thr 40 Cys	Tyr Ser 25 Ile Asj	Thr 10 Trp Arco Valu Leu 1 Va. 90	Thr Met Lev 1 Lev 75	Pro Pro 60	. Met / Gl; Ph 45 Va t Va e Se	y Phe 30 e Cy:	r Arg 15 e Val e Ly r As r Ty 95	Gl: Gl: Hi Hi Fr Ref Ref Ref Ref Ref Ref Ref Re	y s o o		

Ser Phe Ile Tyr Pro His Pro Phe Ser Thr Phe Ser Val Asp Lys Met 130 135 140

<210: <211: <212: <213:	> 4 > D	09 88 NA alli	thri:	x ja	cchus	5											
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att Ile	tgt Cys	gtc Val	acg Thr 20	atg Met	att Ile	ata Ile	gtt Val	tgt Cys 25	tgg Trp	tcc Ser	att Ile	agc Ser	ata Ile 30	gct Ala	GJ ^A aaa	9'	7
gcc Ala	ctg Leu	atc Ile 35	ctc Leu	act Thr	gtc Val	ttc Phe	acc Thr 40	atg Met	cat His	ctg Leu	cct Pro	tat Tyr 45	tgt Cys	ggc Gly	ccc Pro	14	5
tac Tyr	aag Lys 50	ata Ile	aac Asn	cac His	ttc Phe	ttc Phe 55	tgt Cys	gag Glu	gtc Val	cct Pro	gct Ala 60	gtc Val	ctg Leu	aag Lys	ttg Leu	19	3
gcc Ala 65	tgt Cys	gca Ala	gac Asp	aca Thr	tct Ser 70	ttt Phe	aat Asn	gac Asp	agg Arg	ctg Leu 75	gac Asp	ttc Phe	atc Ile	ttg Leu	ggt Gly 80	24	:1
ttc Phe	ato	ctg Leu	ctt Leu	ttg Leu 85	gtc Val	cca Pro	ctc Leu	tcc Ser	ctc Leu 90	atc Ile	ctg Leu	gcc Ala	tct Ser	tac Tyr 95	gtc Val	28	}9
ttc Phe	atc Ile	ttt Phe	gcc Ala 100	tct Ser	atc Ile	ttc Phe	aga Arg	atc Ile 105	cgc Arg	tca Ser	gcg Ala	cag Gln	ggg Gly 110	agg Arg	ctc Leu	33	37
aag Lys	tcc Ser	ttc Phe	Ser	acg Thr	tgt Cys	gct Ala	tcc Ser 120	His	gtc Val	act Thr	gtg Val	gtc Val 125	acc Thr	atg Met	ttc Phe	38	85
tat Tyr	999 Gl ₃	Pro	gcc Ala	atc Ile	atc Ile	atg Met 135	Tyr	atg Met	agg Arg	ccc Pro	ggt Gly 140	tct Ser	tgg Trp	tat Tyr	gac Asp	43	33
cca Pro 145	Glı	g cgg ı Arg	gac J Asp	aag Lys	aag Lys 150	Leu	gcg Ala	r ctg Leu	tto Phe	tac Tyr 155	aat Asn	gtg Val	gtc Val	tct Ser	ggc Gly 160	4:	81

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<213> Callithrix jacchus

<220>

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<222> (1)..(488)

<223> Taxon = 9483; gene = CJA201; Accession DDBJ/EMBL/GenBank = AF179810

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Ile Cys Val Thr Met Ile Ile Val Cys Trp Ser Ile Ser Ile Ala Gly 20

Ala Leu Ile Leu Thr Val Phe Thr Met His Leu Pro Tyr Cys Gly Pro 40

Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu 55

Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly 70

Phe Ile Leu Leu Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Val

Phe Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Ala Gln Gly Arg Leu 105

Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe 120

Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp

Pro Glu Arg Asp Lys Lys Leu Ala Leu Phe Tyr Asn Val Val Ser Gly 145 150

Phe Leu

<210> 311

<211> 487

<212> DNA

<213> Callithrix jacchus

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<222> (2)..(487)
<223> Product = olfactory receptor
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                                                                       49
 Val Ala Ile Cys His Pro Leu Arg Tyr Thr Ala Thr Met Asn Leu Arg
ctt tgt gtc cag cta gtg gct gga ctg tgg ctt gtt act tac ctc cat
                                                                       97
Leu Cys Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His
            20
gcc ctc ctg cat act tcc cta ata gca cat ctg tcc ttc tgt gcc ttc
                                                                      145
Ala Leu Leu His Thr Ser Leu Ile Ala His Leu Ser Phe Cys Ala Phe
                            40
aat atc atc cat cat ttc ttc tgt gat ctc aac cct cta cta cgg ctc
                                                                      193
Asn Ile Ile His His Phe Phe Cys Asp Leu Asn Pro Leu Leu Arg Leu
tot tgo tot goo gto too tto aac gta atg atc att ttt goa gta gga
                                                                      241
Ser Cys Ser Ala Val Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly
ggt cta ttg gct ctc acg ccc ctt gtc tgt atc ctc gta ttt tat gga
                                                                      289
Gly Leu Leu Ala Leu Thr Pro Leu Val Cys Ile Leu Val Phe Tyr Gly
                                                                       337
ctt atc ttc tcc act gtt ctg aag atc acc tct act cag ggg aaa cag
Leu Ile Phe Ser Thr Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln
                                 105
 aga gct gct tcc acc tgc ggc tgc cac ctg tca gta gtg gtg ctg ttt
                                                                       385
 Arg Ala Ala Ser Thr Cys Gly Cys His Leu Ser Val Val Val Leu Phe
 tat ggc aca gcc att gcc gtc tac ttt agc ccc tca tcc tcc cat acg
                                                                       433
 Tyr Gly Thr Ala Ile Ala Val Tyr Phe Ser Pro Ser Ser His Thr
                         135
     130
 cet gag agt gac act etc teg ace gte atg tat tea gtg gtg gee eeg
                                                                       481
 Pro Glu Ser Asp Thr Leu Ser Thr Val Met Tyr Ser Val Val Ala Pro
                                                              160
 145
                                                                       487
 atg ctg
 Met Leu
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Leu Cys Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His 20 25 30

Ala Leu Leu His Thr Ser Leu Ile Ala His Leu Ser Phe Cys Ala Phe 35 40 45

Asn Ile Ile His His Phe Phe Cys Asp Leu Asn Pro Leu Leu Arg Leu 50 60

Ser Cys Ser Ala Val Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly 65 70 75 80

Gly Leu Leu Ala Leu Thr Pro Leu Val Cys Ile Leu Val Phe Tyr Gly $85 \hspace{1.5cm} 90 \hspace{1.5cm} 95$

Leu Ile Phe Ser Thr Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln 100 $\,$ 105 $\,$ 110 $\,$

Arg Ala Ala Ser Thr Cys Gly Cys His Leu Ser Val Val Leu Phe 115 120 125

Tyr Gly Thr Ala Ile Ala Val Tyr Phe Ser Pro Ser Ser Ser His Thr $130\,$

Pro Glu Ser Asp Thr Leu Ser Thr Val Met Tyr Ser Val Val Ala Pro 145 150 155

Met Leu

<400> 312

<210> 313
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= AF179812

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cctttcactg ggtgtctatg ggatggggt ttttggggct gtggttcata tgggaaacat 120
aatgtttatg tccttttgtg gagacaacct tgtcaatcac tatctgtgtg acatccttcc 180
tctccttgag ctctcctgca acagctctta cataaatttg ctggtggttt ttattattgt 240

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gaccattggc attggggtgc caattgtcac catttttatc tettatggtt ttattettte
                                                                     300
cagcattete cacattaget cacagaggge aggteaggte taaageette agtacetgea
                                                                     360
gttcccacat aattgtggta tcgcttttct ttgggtcagg tgctttcatg tacctcaaac
                                                                     420
caccttetet tetacecetg gaccagggga aagtgteete cattttttat aetgetgtgg
                                                                     480
tgcccatgtt t
                                                                     491
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      314
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      DNA
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= AF179813
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                                                                      60
cccttttggc gctgtcctgg gtgctgacca ccttccatgc catgttacac actttactca
                                                                     120
tggccaggtt gtgtttttgt gcagacaatg tgatccccca ctttttctgt gatatgtctg
                                                                     180
ctctgctgaa gctgtcctgc tctgacactc gagttaatga attggtgata tttatcatgg
                                                                     240
gagggeteat tettgteate ceatteetae teateettgg gteetatgea egaattgtet
                                                                     300
cctccatcct caaggtccct tctaagggta tctgcaaggc cttctctact tgtggctccc
                                                                     360
acctetetqt qgtqteeetg ttetatggga cegttagtgg tetetaetta tgcccategg
                                                                     420
                                                                      480
ctaataqttc tactctgaag gagactgtca tggctgtaat gtacactgtg gtgaccccca
<210> 315
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       486
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<221> misc_feature
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<221> CDS
<222>
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<223> Product = olfactory receptor
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                                                                       48
Cys Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
                                    10
cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
                                                                       96
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
            20
get ett ttg eat acc etc ett etg gee egg ett tee tte tgt get gae
                                                                      144
Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
```

	35				40					45				
cac atc His Ile 50	atc t Ile S	ct ca er Hi	ac tto Is Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu	192
tcc tgc Ser Cys 65	tca g Ser A	ac ac .sp Th	cc tcc nr Ser 70	ctc Leu	aat Asn	cag Gln	tta Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80	240
ttg aca Leu Thr	gcc a Ala I	tt at le Me 8!	et Lei	cca Pro	ttc Phe	ctg Leu	tgc Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly	288
cac att His Ile	Gly V	rtc ao Mal Ti .00	cc ato hr Ile	ctc Leu	cag Gln	att Ile 105	ccc Pro	tcc Ser	acc Thr	aag Lys	ggc Gly 110	ata Ile	tgc Cys	336
aaa gcc Lys Ala	ttg t Leu S 115	cc a Ser T	ct tgt hr Cy:	gga Gly	tcc Ser 120	cac His	ctc Leu	tca Ser	gtg Val	gtg Val 125	act Thr	atc Ile	tat Tyr	384
tat ggg Tyr Gly 130	aca a Thr I	att a [le I	tt gg le Gl	t ctc y Leu 135	Tyr	ttt Phe	cta Leu	ccc Pro	cca Pro 140	ser	agc Ser	aac Asn	acc Thr	432
aat gac Asn Asp 145	aag a Lys <i>l</i>	aac a Asn I	ta at le Il 15	e Ala	tca Ser	gtg Val	ata Ile	tac Tyr 155	Thr	gta Val	gtc Val	act Thr	ccc Pro 160	480
atg ttg Met Leu														486
<211> <212>	316 162 PRT Pongo	pygr	naeus											
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<400>	316													
Cys Ala 1	a Ile	Cys I	His Pı 5	o Le	u Hi	в Туі	Ala 10	a Thi	r Ile	e Met	t Se:	r Gl: 15	n Ser	
Gln Cys	s Val	Met 1	Leu Va	al Al	a Gl	y Se: 25	r Tr	p Va	l Il	e Ala	а Су 30	s Al	a Cys	
Ala Lei	u Leu 35	His	Thr L	eu Le	u Le 40		a Ar	g Le	u Se	r Ph 45	е Су	s Al	a Asp	
His Ile	e Ile	Ser	His P	he Ph		s As	p Le	u Gl	y Al 60	a Le	u Le	u Ly	s Leu	

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

<222>

(1)..(484)

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Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                                     90
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
                            120
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                    150
                                         155
Met Leu
<210> 317
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= AF179815
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cactgccatt tgccaccctc taagataaac caatctcatg agacccaaaa tttgtggact
                                                                       120
tatgactgcc ttctcctgga tcctgggctc tacggatgga atcattgatg ctgcagcgac
attttccttc tcctactgtg ggtctcggga aatagcccac ttcttctgtg agttcccttc
                                                                       180
catactaatc ctctcatgca atgacacatc aatatttgaa aaggttcttt tcatctgctg
                                                                       240
                                                                       300
tatagtaatg attgttttc ctgttgcaat catcatcgct tcctatgctc aagttattct
                                                                       360
qqctqtcatt cacatqqgat ctggagaggg tcgtcggata gctttcacga cctgttcctc
                                                                       420
tcacctcatg gtggtgggaa tgtactatgg agcagctttg ttcatgtaca tacggcccac
                                                                       480
atctgatcgc tecectacae aggacaagat ggtgtetgta ttetacaeca tecteaetee
                                                                       487
catgctg
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<223> Taxon = 9600; gene = PPY114; Accession DDBJ/EMBL/GenBank = AF179816

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t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg
                                                                       49
  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
                                      1.0
ctc tgt ctc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
                                                                       97
Leu Cys Leu Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
            20
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac
                                                                      145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
                                                                       193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
    50
tee tge tet gae act ega gtt aat gaa ttg gtg ata ttt ate atg gga
                                                                       241
Ser Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
ggg ctc att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca
                                                                       289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                 85
                                                                       337
cga att gtc tcc tcc atc ctc aag gtc cct tct aag ggt atc tgc aag
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys
                                                      110
gcc ttc tct act tgt ggc tcc cac ctc tct gtg gtg tcc ctg ttc tat
                                                                       385
 Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
                                                  125
         115
                             120
 ggg acc gtt agt ggt ctc tac tta tgc cca tcg gct aat agt tct act
                                                                       433
 Gly Thr Val Ser Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr
     130
 ctg aag gag act gtc atg gct gta atg tac act gtg gtg acc ccc atg
                                                                        481
 Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Val Thr Pro Met
                                                              160
                                          155
                     150
 145
                                                                        484
 ctg
 Leu
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 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
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1.0

Leu Cys Leu Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 25

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu

Ser Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 70

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 85

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys 105 100

Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr 120

Gly Thr Val Ser Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr 135

Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Val Thr Pro Met 155

Leu

<210> 320

<211> 483

<212> DNA <213> Pongo pygmaeus

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96 Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn 20

tee etg atg gaa aca att ate ace tte eag ett ete etg tgt eac aat 144

Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Leu Cys His Asn 35 40 45	
gtt att aat cac ttt gcc tgt gag acc tta gca gtg cta cga cta gcc 192 Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala 50 55 60	
tgt gtg gac gtc tcc ttc aac aag gcc atg gtg gcc atc tca ggg ttt 240 Cys Val Asp Val Ser Phe Asn Lys Ala Met Val Ala Ile Ser Gly Phe 65 70 75 80	
ctg gtg atc ctg ctt ccc tgt tca ctg atc cta ttc tcc tat gct cac 288 Leu Val Ile Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His 85 90 95	
ata gtt gct gcc att ctt cat att cct tct gcc cag gga cgc cgc aaa 336 Ile Val Ala Ala Ile Leu His Ile Pro Ser Ala Gln Gly Arg Arg Lys 100 105 110	
gcc ttt ggg act tgc acg tct cac ctc act gtg gtt tgc atg tgc ttt 384 Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe 115 120 125	
ggg gct aca atg ttc acc tac atg aga cct gcg ggc ggc tcc tcc ctg Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu 130 135 140	
gaa aag aag aat atg gtt gcc ctc ttt tat gcc att gtg att cca atg Glu Lys Lys Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met 145 150 160	
ctt Leu	
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Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn 20 25 30	
Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Leu Cys His Asn 35 40 45	
Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala 50 55 60	

Leu Va	l Ile		Leu I 85	?ro (Cys S	er I	Leu	Ile 90	Leu	Phe	Ser	Tyr	Ala 95	Hi	.s	
Ile Va	l Ala	Ala 100	Ile 1	Leu I	His I		Pro 105	Ser	Ala	Gln	Gly	Arg 110	Arg	, ГУ	/S	
Ala Ph	e Gly 115	Thr	Cys '	Thr :	Ser H	His :	Leu	Thr	Val	Val	Cys 125	Met	Сув	s Pł	ie	
Gly Al		Met	Phe '	Thr '	Tyr N 135	Met	Arg	Pro	Ala	Gly 140	Gly	ser Ser	Ser	c Le	eu	
Glu Ly 145	s Lys	Asn	Met	Val 150	Ala 1	Leu	Phe	Tyr	Ala 155	Ile	· Vai	l Il∈	e Pro	O M	et 60	
Leu																
<210><211><212><212><213>	484 DNA	lo by	gmaeı	ıs												
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<220><221><222><223>	CDS	(48 duct	4) = ol	fact	ory 1	cece	ptor	ĵ								
<400> t gtg Val 1		gtc t Val C	gc c ys H	is P	ca ci ro Le	tg c eu H	at t is T	ryr :	acg (Thr 1	ctc Leu	atc Ile	atg Met	cat His	999 Gl: 15	a ggg y Gly	49
	gc ct ys Le	g ggg u Gly 20	g ctg r Leu	gtg Val	gcc Ala	ggc	tgo Cy: 25	c ct	g gt u Va	g go l Al	t g a G	gt tt ly Ph 30		tg et .	aat Asn	97
tcc (Ser I	ctg at Leu Me	t Gli	a aca ı Thr	att : Ile	atc :Ile	acc Thr 40	tt.	c ca e Gl	g ct n Le	t co u Pi	cc c co L 4	eu c	gt c ys H	ac is	aat Asn	145
Val :	att aa [le As	it cad sn His	c ttt s Phe	gco Ala	tgt Cys 55	gag	g ac ı Th	c tt r Le	a go u Al	a gt a Va	ם בג	ta c eu A	ga c rg L	ta eu	gcc Ala	193
tgt Cys 65	gtg ga Val A	ac gte sp Va	c tco l Sei	tto Phe 70	aac Asn	aaq Ly	g gc s Al	c ac a Th	g gt ir Va 75	II A	cc a la I	tc t le S	ca g er G	gly	ttt Phe 80	241
ctg Leu	ata a	c ct	a cti	t cc	c tat	t c	a ct	g at	c ct	at	tc t	.cc t	at g	gct	cac	289

ata gtt gct gcc att ctt cgt att cct tct gcc cag gga cac cgc aaa Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Gln Gly His Arg Lys 100 105 110	37
gcc ttt ggg acc tgc acg tct cac ctc act gtg gtt tgc atg tgc ttt Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe 115 120 125	885
ggg gct aca atg ttc acc tac atg aga cct gcg ggt ggc tcc tcc ctg Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu 130 135 140	133
gaa aag gag aat atg gtt gcc ctc ttt tat gcc att gtg att cca atg Glu Lys Glu Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met 145 150 155 160	181
ctt Leu	484
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Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn 20 25 30	
Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Leu Cys His Asn 35 40 45	
Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala 50 55 60	
Cys Val Asp Val Ser Phe Asn Lys Ala Thr Val Ala Ile Ser Gly Phe 65 70 75 80	
Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His 85 90 95	
Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Gln Gly His Arg Lys 100 105 110	
Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe 115 120 125	
Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu	

130 135 140

Glu Lys Glu Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met 145 150 155

Leu

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= AF179819
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tgtgaacctg ccttttttgt ggacctaatg tagtagacag ctttttttgt gatcttcctc
                                                                     180
gagtgaccaa acttgcctgc ctggactctt acctcattga aatactaatt gtggtcaata
                                                                      240
gtggagttct ttccctaagc actttctgtc tcttggtcag ctcctacatc attattcttg
                                                                      300
ttatggtttg gctcaagtct tcggctgcaa tggcgaaggc attttctacg ctggcttccc
                                                                      360
atattgcagt agtaatatta ttctttggac cttgcatctt catctatgtg tggcccttta
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ccatctatcc tttggataaa cttcttgcca tattttacac tgttttcacc cccatccta
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 cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
                                                                       97
 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
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145

get ett ttg cat acc etc ett etg gee egg ett tee tte tgt get gae

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp

		35					40					45					
cac His	atc Ile 50	atc Ile	tct Ser	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu		193
tcc Ser 65	tgc Cys	tca Ser	gac Asp	acc Thr	tcc Ser 70	ctc Leu	aat Asn	cag Gln	tta Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80		241
ttg Leu	aca Thr	gcc Ala	att Ile	atg Met 85	ctt Leu	cca Pro	ttc Phe	ctg Leu	tgc Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly		289
cac His	att Ile	Gly aaa	gtc Val 100	acc Thr	atc Ile	ctc Leu	cag Gln	att Ile 105	ccc Pro	tcc Ser	acc Thr	aag Lys	ggc Gly 110	ata Ile	tgc Cys		337
aaa Lys	gcc Ala	ttg Leu 115	tcc Ser	act Thr	tgt Cys	gga Gly	tcc Ser 120	cac His	ctc Leu	tca Ser	gtg Val	gtg Val 125	act Thr	atc Ile	tat Tyr		385
tat Tyr	999 Gly 130	aca Thr	att Ile	att Ile	ggt Gly	ctc Leu 135	tat Tyr	ttt Phe	ctt Leu	ccc Pro	cca Pro 140	tcc Ser	agc Ser	aac Asn	acc Thr		433
aat Asn 145	Asp	aag Lys	aac Asn	ata Ile	att Ile 150	gct Ala	tca Ser	gtg Val	ata Ile	tac Tyr 155	Thr	gta Val	gto Val	act Thr	ccc Pro 160		481
_	ttg Leu																487
	1> 12>	326 162 PRT Pong	lo b?	/gmae	eus												
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Va 1	l Ala	a Ile	е Су	s His 5	s Pro) Le	ı Hi:	s Ту:	r Ala 10	a Thi	r Il	e Met	Se:	r Gl: 15	n Ser		
Gl:	n Cy	s Va	1 Me 20		u Vai	l Ala	a Gl	y Se: 25	r Tr	p Va	1 I1	e Ala	а Су 30	s Al	a Cys		
Al	a Le	u Le 35	u Hi	s Th	r Le	u Le	u Le 40	u Al	a Ar	g Le	u Se	r Ph 45	е Су	s Al	a Asp		
Hi	s Il 50		e Se	r Hi	s Ph	e Ph 55	е Су	s As	p Le	u Gl	y Al 60	a Le	u Le	u Ly	s Leu		
Se 65		s Se	r As	p Th	r Se	r Le	u As	n Gl	n Le	u Al 75	a Il	e Ph	e Th	ır Al	a Gly 80		

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Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
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Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
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Met Leu
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 gtaagcttgc ccttctgtgg cccaaacata gtggacagtt attattgcga ccttactttg
                                                                       180
 gtcatcaaac gtgcctgtac agatgcttat atccctgaag tgttgatgct tttggacggt
                                                                       240
 ggtcttatgg gggtgaccat ttttgctttt gctgatctcc tacacggtca ttctgattac
                                                                       300
 tgtgcagcga cattcctcag caggtatggc caaggctcac agcactctga ctgcccacat
                                                                       360
 tgctgtggtg accgtgttct ttgggccctg tatcttcatc tatgcctggc ctttcagcaa
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cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30	97										
gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp 35 40 45	145										
cac atc atc cct cac ttc ttc tgc gac ctt ggt gcc ctg ctc aag ctg His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60	193										
tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80	241										
ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95	289										
cac att ggg gtc acc atc ctc cag att ccc tcc acc aag ggc ata tgc His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100 105 110	337										
aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125	385										
tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140	433										
aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 155	481										
atg ttg Met Leu	487										
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Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 105

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 120

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 140 135

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 155

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<223> Product = olfactory receptor

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ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser 20

tec etc tet cac acc ett etg etg acc eeg etg eet tte tgt gat gea 145 Ser Leu Ser His Thr Leu Leu Thr Pro Leu Pro Phe Cys Asp Ala 35

97

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60	193
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80	241
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95	289
tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110	337
aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr 115 120 125	385
tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135	433
att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 160	481
atg ctg Met Leu	487
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	AF179823
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Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95	
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110	
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr 115 120 125	
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140	
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155 160	
Met Leu	
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ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser 20 25 30	97
tcc ctc tct cac acc ctt ctg ctg acc ccg ctg tct ttc tgt gat gca Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala 35 40 45	145
aac acc gtc cac cac tac ttc tgt gac ctt gct gcc ctg ctc aag ctg Asn Thr Val His His Tyr Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60	193
tcc tgc tca gat atc ttc ctc aac gag ctg gtc atg ttc aca gta ggg Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80	241

289

337

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95

tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg

100 105 110

	ttg Leu 115									385
	tca Ser									433
_	aag Lys	_	_		_			 _		481
 ctg Leu	t									488

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<400> 333

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Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala

Asn Thr Val His His Tyr Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser

Met Leu											
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ctc tgc agc ctg ctg att ctt ctt tct ccg ttg act agc gtt gtg aat Leu Cys Ser Leu Leu Ile Leu Leu Ser Pro Leu Thr Ser Val Val Asn 20 25 30	97										
gcc ctt ctt ctc agc ctg atg gtg ttg agg ctg tcc ttc tgc aca gat Ala Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp 35 40 45	145										
ctg gaa atc ccg ctc ttc ttc tgt gaa ctg gct cag gtc atc cag ctt Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu 50 55 60	193										
gct tgt tct gac acc ctc atc aat aac atc ctg ata tat ttt gca gct Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala 65 70 75 80	241										
tgc ata ttt ggt ggt gtt cct ctg tct gga atc ata ttc tct tat gct Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala 85 90 95	289										
cag att gcc tcc tct att ttg aga atg cca tca gca cgc aga aag tat Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr 100 105 110	337										
aaa gcc ttt tcc acc tgt ggg tct cac ctc tcc atg gtg ctc ttg ttc Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe 115 120 125	385										
tat agg aca ggt ttg ggg gtg tac att agt tct gca gtt act gac tca Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser 130 135 140	433										
cct agg aag act gca gtg gct tca atg atg tat tct gtg ggt cct caa Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln 145 150 155 160	481										
atg gtg	487										

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Val

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Ala Leu Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp
                            40
Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu
    50
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala
Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala
Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr
                                                     110
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe
                             120
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 Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser
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 Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln
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 Met Val
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<400> 337

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ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
                                                                       97
Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
gcc atg ttg cac act tta ctc atg gcc agg ttg cgt ttt tgt gca gac
                                                                      145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp
                            40
aat gtg atc ctc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
                                                                      193
Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
                                                                      241
gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
                    70
                                        75
                                                                      289
ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc
                                                                      337
Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
                                105
aag goo gto tot act tgt ggo too cac ctc tot gtg gtg toa ctg tto
                                                                      385
Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
                            120
                                                                      433
tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
                        135
                                                                      481
act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc
Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
                                         155
                                                                      487
atg ctg
Met Leu
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Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
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Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp

Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu

Ala Cys Ser Asp Thr Arq Val Asn Glu Leu Val Ile Phe Ile Met Gly 70

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala 85

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser 130 135 140

Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro 145 150 155

Met Leu

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<213> Saimiri sciureus

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atc tgc ctg cag ctt gtg ctt ggg tgc tgg gtt ctt ggt ttt ctc atc

97

Ile	Cys	Leu	Gln 20	Leu	Val	Leu	Gly	Cys 25	Trp	Val	Leu	Gly	Phe 30	Leu	Ile		
		cca Pro 35														145	
	-	gtt Val	_					_			_		_	_		193	
	_	aca Thr	~	. ~			_									241	
_		aca Thr			-		_	_		_						289	
		gcc Ala														337	
		ttt Phe 115														385	i
tat Tyr	ggc Gly 130	agc Ser	tgc Cys	atc Ile	ttc Phe	atg Met 135	tat Tyr	gtt Val	aag Lys	cca Pro	tca Ser 140	gtc Val	aaa Lys	caa Gln	agg Arg	433	;
gta Val 145	tct Ser	ttt Phe	tca Ser	aag Lys	gga Gly 150	att Ile	tcg Ser	gtg Val	ctc Leu	aat Asn 155	acc Thr	tct Ser	gtt Val	gct Ala	cca Pro 160	481	
	ttg Leu															487	7
<21 <21 <21 <21	1> 2>	339 162 PRT Saim	iri	sciu	reus												
<22 <22 <22 <22	1> 2>		.(48	7)		ne =	SSC	190;	Acc	essi	on D	DBJ/	EMBL	/Gen	Bank :	= AF1798	327
<40	0>	339															
Val 1	Ala	Ile	Cys	Lys 5	Pro	Leu	His	Tyr	Thr 10	Thr	Ile	Met	Ser	Ser 15	Lys		
Ile	Cys	Leu	Gln 20	Leu	Val	Leu	Gly	Cys 25	Trp	Val	Leu	Gly	Phe 30	Leu	Ile		
Ile	Phe	Pro 35	Pro	Leu	Leu	. Leu	Gly 40	Leu	Asn	. Leu	Asp	Phe 45	Cys	Ala	Ser		
Asn	Val	Val	Asp	His	Phe	Tyr 55	Phe	Asp	Thr	·Ile	Pro	Leu	Leu	Gln	Ile		

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Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
                25
Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
                                105
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
Leu Leu
<210> 340
<211> 485
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<213> Saimiri sciureus
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 <223> Product = olfactory receptor
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 Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly
 tac tgt gga cag ctg gtg gct ttc tct tac atg agt ggt ttc atg atc
                                                                        96
 Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile
 tot gto ato aag gto tat tto att toa cat gtt got tto tgt ggo too
                                                                       144
 Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser
         35
                              40
 aat gtt atg aac cac ttt ttc tgt gat atc tca cca gtc cta aaa ctg
                                                                       192
 Asn Val Met Asn His Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu
 gca tgc aaa gac atg tcc aca gct gag cta gtg gac ttt gct tta gct
                                                                       240
 Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala
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atc gtc att ctt gtg atc cct ctc att acc act atc ctc tcc tat atc Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile 85 90 95	288
tac att gtc tcc gcc att ctg cat ata ccc tcc acc cag gga agg aag Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys 100 105 110	336
aag gcc ttc tcc acc tgt gca tct cac ctc act gta gtc ata att ttt Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe 115 120 125	384
tac aca gcc atg att ttt aca tat gtt cgg ccc aga gct att gca tca Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser 130 135 140	432
ttt aat tcc aac aaa cta atg tca gct gtg tat gca gtc ctc aca ccc Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro 145 150 160	480
atg ct Met	485
<210> 341 <211> 161 <212> PRT <213> Saimiri sciureus <220> <221> misc feature	
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-222 (1) (485)	F179828
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<pre><222> (1)(485) <223> Taxon = 9521; gene = SSC191; Accession DDBJ/EMBL/GenBank = A <400> 341 Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly 1</pre>	F179828
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Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe

115 120 125

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser $130\,$

Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro 145 150 155 160

Met

<210><211><212><213>	342 487 DNA Saimi	ri s	ciur	eus											
<220><221><222><223>	misc_ (1) Taxon	(487)	gen	e = -	SSC1	92;	Acce	ssio	n DDi	BJ/El	MBL/	GenB:	ank = F	AF179829
<220><221><222><222><223>	CDS (2) Produ			acto	ry r	ecep	tor								
<400> t gtt Val 1	342 gcc at Ala Il	a tg .e Cy	t ta s Ty 5	c cc r Pr	t ct o Le	c ca u Hi	c ta s Ty	c ac r Th 10	r Al	c at a Il	c at e Me	g ag t Ar	g ga g Gl 15	u Giy	49
ctc to	gt gcc ys Ala	ttc Phe 20	tta Leu	gtg Val	gct Ala	gta Val	tct Ser 25	tgg Trp	att Ile	cca Pro	tct Ser	tgt Cys 30	gct Ala	agc Ser	97
tcc ct Ser Le	tc tct eu Ser 35	cac His	acc Thr	ctt Leu	ctg Leu	ctg Leu 40	acc Thr	ccg Pro	ctg Leu	tct Ser	ttc Phe 45	tgt Cys	gat Asp	gca Ala	145
aac ac Asn Tl	cc gtc hr Val 0	cac His	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	gct Ala	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu	193
tcc to Ser C	gc tca ys Ser	gat Asp	atc Ile	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 GJA 333	241
gtg g Val V	tg gtc al Val	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggc Gly	289
tac a Tyr T	.ct ggg hr Gly	gcc Ala 100	act Thr	atc Ile	ctg Leu	agg Arg	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	999 Gly 110	atc Ile	cgc Arg	337
aaa g Lys A	gcg ttg Mla Leu 115	Ser	atg Met	tgt Cys	ggc	tcc Ser 120	cgt Arg	ctc Leu	tct Ser	gtg Val	gtg Val 125	tct Ser	ctg Leu	tat Tyr	385
Tyr G	ggc tca Bly Ser	ata Ile	ttt Phe	ggc Gly	cag Gln 135	Tyr	ctt Leu	ttc Phe	cca Pro	act Thr 140	gta Val	agc Ser	agt Ser	tcc Ser	433

att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155 160	181
atg ctg Met Leu	187
<210> 343 <211> 162 <212> PRT <213> Saimiri sciureus	
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Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly 1 5 10 15	
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser 20 25 30	
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala 35 40 45	
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60	
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80	
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 . 95	
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110	
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr 115 120 125	
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140	
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155 160	

Met Leu

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<210> 344
<211> 487
<212> DNA
<213> Saimiri sciureus
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      Taxon = 9521; gene = SSC193; Accession DDBJ/EMBL/GenBank = AF179830
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<221> CDS
<222>
      (2)..(487)
<223> Product = olfactory receptor
<400> 344
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                                                                       49
  Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc
                                                                       97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
                                                                      145
tee etc tet cae ace ett etg etg ace eeg etg tet tte tgt gat gea
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg
                                                                      193
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
                        55
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg
                                                                      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
                     70
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc
                                                                      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                     90
 tac act ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cgc
                                                                       337
 Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
                                 105
 aaa geg ttg tee atg tgt gge tee egt ete tet gtg gtg tet etg tat
                                                                       385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
                                                 125
                             120
 tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc
                                                                       433
 Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
 att gac aag gat gtc att gtg gct cta acg tac aca gtg gtc aca ccc
 Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro
                                                              160
 145
                     150
                                                                       487
 atg ctg
 Met Leu
 <210> 345
 <211> 162
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<212> PRT

<213> Saimiri sciureus

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<220>
<221> misc_feature
<222>
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<223> Taxon = 9521; gene = SSC193; Accession DDBJ/EMBL/GenBank = AF179830
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Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
                               25
           20
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
                            40
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
                                105 110
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
        115
                            120
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
    130
Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro
                    150
145
Met Leu
<210> 346
<211> 486
<212> DNA
 <213> Saimiri sciureus
 <220>
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 <222> (1)..(486)
 <223> Taxon = 9521; gene = SSC194; Accession DDBJ/EMBL/GenBank = AF179831
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 <221> CDS
 <222> (2)..(484)
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<223> Product = olfactory receptor

<400 t gt Va	a ac	46 c at a Il	c tg e Cy	t ca s Hi	c cc s Pr	c ct o Le	g ca u Hi	c ta s Ty	c ac r Th	a gt r Va	c ac l Th	c at r Il	t aa e As	n Pr	c aga o Arg		49
1 ctg Leu	tgt Cys	gga Gly	ctg Leu 20	5 ctg Leu	gtt Val	ctg Leu	gca Ala	tcc Ser 25	10 tgg Trp	atc	ctg Leu	agt Ser	gcc Ala 30	15 ctg Leu	aat		97
tcc Ser	tca Ser	tta Leu 35	caa Gln	acc Thr	tta Leu	Ile	gtg Val 40	ctg Leu	cgg Arg	ctt Leu	tcc Ser	ttc Phe 45	tgc Cys	aca Thr	gac Asp		145
ttg Leu	gaa Glu 50	atc Ile	ccc Pro	cac His	ttt Phe	ttc Phe 55	tgc Cys	gaa Glu	ctt Leu	aat Asn	cag Gln 60	gtc Val	ata Ile	cat His	ctt Leu		193
gcc Ala 65	tgt Cys	tat Tyr	gac Asp	act Thr	ttc Phe 70	ctt Leu	aat Asn	gat Asp	gtg Val	gtg Val 75	atg Met	tat Tyr	ttg Leu	gca Ala	gct Ala 80		241
atg Met	ctg Leu	ctg Leu	ggc Gly	ggt Gly 85	ggt Gly	ccc Pro	ctc Leu	aca Thr	gga Gly 90	att Ile	att Ile	tac Tyr	tct Ser	tac Tyr 95	tct Ser		289
aag Lys	ata Ile	gtt Val	tcc Ser 100	tcc Ser	ata Ile	cgt Arg	gca Ala	atc Ile 105	tca Ser	tca Ser	gct Ala	cag Gln	999 Gly 110	aag Lys	tac Tyr		337
aag Lys	gcg Ala	ttt Phe 115	tcc Ser	acc Thr	tgt Cys	gca Ala	tct Ser 120	cac His	atc Ile	tta Leu	att Ile	gtc Val 125	tcc Ser	tta Leu	ttt Phe		385
tat Tyr	ggt Gly 130	Thr	ctc Leu	cta Leu	ggt Gly	gtg Val 135	tac Tyr	att Ile	agt Ser	tct Ser	gct Ala 140	gca Ala	act Thr	ggc Gly	aac Asn		433
tca Ser 145	His	tca Ser	agt Ser	gct Ala	gca Ala 150	Ala	ttg Leu	gtg Val	atg Met	tac Tyr 155	act Thr	gtg Val	gtc Val	acc Thr	ccc Pro 160		481
atg Met	ct																486
<21 <21 <21 <21	.1> .2>	347 161 PRT Sain	niri	sciu	ıreus	\$											
<22	20> 21> 22> 23>	(1)	- (15	ature 36) 9521		ene =	= SS(C194;	· Acc	cessi	on I	DBJ,	/EMBI	ے/Ger	nBank	= AI	F179831
<40	00>	347															
Va:	l Ala	a Ile	e Cy:	s His 5	s Pro) Let	ı His	з Туі	r Thi	. Val	. Thi	r Ile	e Asr	n Pro 15	o Arg		
Le	u Cy	s Gl	y Le 20	u Lei	ı Va	l Leı	ı Ala	a Se: 25	r Trj	o Ile	e Lei	ı Se:	r Ala 30	a Lei	u Asn		

Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu 55

Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala 70

Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr 100

Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe 120

Tyr Gly Thr Leu Leu Gly Val Tyr Ile Ser Ser Ala Ala Thr Gly Asn 130 135

Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro 155

Met

<210> 348

<211> 487

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)
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<220>

<221> CDS <222> (2)..(487)

<223> Product = olfactory receptor

<400> 348

c gtg gcc atc tgt aac cca ctg ctg tac atg gtc acc atg tct ccc cag Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln 49

gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg 97 Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly

gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa 145 Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu 40

aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc 193 Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu

tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Phe Ile Ile Val

gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 90

ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct 337 Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser 105 100

241

289

aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe 385 120

ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc 433 Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 130

ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg ccc 481 Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 155

487 atg ttt Met Phe

<210> 349

<211> 162

<212> PRT

<213> Saimiri sciureus

<220>

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(1)..(487) <222>

<223> Taxon = 9521; gene = SSC195; Accession DDBJ/EMBL/GenBank = AF179832

<400> 349

Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln

Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly

Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu 35

Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val

Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 90

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Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
                                105
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
                        135
    130
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
                                        155
                    150
Met Phe
<210> 350
<211> 486
<212> DNA
<213> Saimiri boliviensis
<220>
<221> misc feature
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= AF179833
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                                                                       60
gatgattgga ggctcttgga cgctggggtc catcaactcc ttggcacaca cagtctatgc
                                                                      120
cetecatatt ecetactgca ggtetagage cattgaccat ttettetgcg acateceage
                                                                      180
 catgttgctt ctcgcctgta cggacacttg ggtctatgaa tacatggttt ttctaagtac
                                                                      240
 aagetgeett eteetettte ttteettgge ateacegett eetatggeeg agteetattt
                                                                      300
 gctgtctacc atacgcattc aaaaaaggga agaaaaaagg cctccaccac catttcaacc
                                                                      360
 catttaactg tagtgatctt ttactatgca ccttttgtct acacctatct tcggcccagg
                                                                      420
 aatetecaet caccateega agacaagate etggeagtet tetacaccat cettaceeet
                                                                      480
                                                                      486
 atgctc
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        351
       487
 <211>
 <212> DNA
 <213> Saimiri boliviensis
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 <221> CDS
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<222> (2)..(487)

<223> Product = olfactory receptor

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atc tgc ctg cag ctt gtg ctt ggg tgc tgg gtt ctt ggt ttt ct Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Le 20 25 30	c atc 97 eu Ile
atc ttt cca cca ctc ctc tta gga cta aat ctt gac ttc tgt gc Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Al 35 40 45	cc tcc 145 .a Ser
aac gtc gtt gat cat ttc tac tgt gac act atc ccg ctc ctg ca Asn Val Val Asp His Phe Tyr Cys Asp Thr Ile Pro Leu Leu Gl 50 55 60	ng att 193 n Ile
tcc tgc aca gac acg cag ctc ctg gag agg atg gga ttc atc tc Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Se 65 70 75	ca gcg 241 er Ala 80
ctg gtg aca ctc tta gtc aca ttg gta atg gtg ata ata tca ta Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Ty 85 90	yr Thr
tat att gcc ctg aca att cta aaa atc cct tca act agt cag ag Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Ar 100 105 110	gg aaa 337 rg Lys
aag gct ttt tcc acg tgt tct tct cac atg att gtg ata tcc ct Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Le 115 120 125	tt tct 385 eu Ser
tat ggc agc tgc atc ttc atg tat gtt aag cca tca gtc aaa ca Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gl 130 135	aa agg 433 ln Arg
gta tot ttt toa aag gga att tog gtg oto aat acc tot gtt go Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val A 145 150 155	ct cca 481 la Pro 160
ctt ttg Leu Leu	487
<210> 352 <211> 162 <212> PRT <213> Saimiri boliviensis	
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Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser S 1 10 1	Ser Lys 15
Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe L 20 25 30	Leu Ile

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Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
```

Asn Val Val Asp His Phe Tyr Cys Asp Thr Ile Pro Leu Leu Gln Ile

Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala 70

Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr

Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys 100

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser 120 115

Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg 135

Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro 150 155

Leu Leu

- <210> 353
- <211> 487
- <212> DNA <213> Saimiri boliviensis
- <220>
- <221> misc_feature
- <222> (1)..(487)
 <223> Taxon = 27679; gene = SBO215; Accession DDBJ/EMBL/GenBank = AF179835
- <220>
- <221> CDS
- <222> (2)..(487)
- <223> Product = olfactory receptor
- <400> 353
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- att tgt gtc aac acg gtc att gtc tgt tgg tcc att agc ata gct ggg 97 Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Ile Ala Gly 20
- gcc ctg atc tac act gtc ttc acc ttg cat ctg cct tat tgt ggc ccc 145 Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cys Gly Pro 40 35
- tac aag ata aac cac ttc ttc tgt gag gtc cct gct gtc ctg aag ttg 193

Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu 50 60	
gcc tgt gca gac aca tct ttt aat gac agg ctg gac ttc att ttg ggt Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly 65 70 75 80	241
ttc ctc ctg ctt ttg gtc cca ctc tcc ttc atc ctg gcc tct tac gta Phe Leu Leu Leu Val Pro Leu Ser Phe Ile Leu Ala Ser Tyr Val 85 90 95	289
ctc atc ttt gcc tct atc ttc aga atc cgc tca gtg cag ggg agg ctc Leu Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Val Gln Gly Arg Leu 100 105 110	337
aag too tto too acg tgt got too cac gtc act gtg gtc acc atg ttc Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe 115 120 125	385
tac gga ccg gcc atc atc atg tac atg agg ccc ggt tct tgg tat gac Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp 130 135 140	433
cca gag tgg gac aag aag gta gag gtg ttg tac aat gtc atc tct gcc Pro Glu Trp Asp Lys Lys Val Glu Val Leu Tyr Asn Val Ile Ser Ala 145 150 155 160	481
ttc ttg Phe Leu	487
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Val Ala Ile Cys Phe Pro Leu His Tyr Thr Leu Leu Met Ser His Ser 15 Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Ile Ala Gly 20 Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cys Gly Pro 45 Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu	

100 105 110
Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe 115 120 125
Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp 130 135 140
Pro Glu Trp Asp Lys Lys Val Glu Val Leu Tyr Asn Val Ile Ser Ala 145 150 150
Phe Leu
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1 5 10 15
= 10 IS
gcc tgc atg acc atg gtg ggc acc tcc tgg ctc aca ggc atc aca aca 97 Ala Cys Met Thr Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr
gcc tgc atg acc atg gtg ggc acc tcc tgg ctc aca ggc atc atc aca Ala Cys Met Thr Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr 20 gcc acc acc cat gcc tcc ctc atc ttc tct ctg ccc ttc ccc agc cac Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Pro Ser His
gcc tgc atg acc atg gtg ggc acc tcc tgg ctc aca ggc atc atc aca Ala Cys Met Thr Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr 20 gcc acc acc cat gcc tcc ctc atc ttc tct ctg ccc ttc ccc agc cac Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Pro Ser His 35 cca atg atc cca cac ttt ctc tgt gac atc ctg cca gta ctg aga ctg Pro Met Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu 15 97 16 17 17 18 97 18 193

cgc atc ctg ggt gcc atc cta gca atg act tcc acc cag agc cgc cac Arg Ile Leu Gly Ala Ile Leu Ala Met Thr Ser Thr Gln Ser Arg His 100 105 110

aag gtc ttc tcc acc tgc tcc tcc cat ctg ctt gtg gtc tgt ctc ttc Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Cys Leu Phe 115 120 125	385
ttt gga aca gcc agc atc acc tac ata cgg ccc cag gca ggc tcc tct Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser 130 135 140	433
gtc acc aca gac cgc atc ctc agt ctc ttc tac acg gtc atc aca ccc Val Thr Thr Asp Arg Ile Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro 145 150 155 160	481
atg ctc Met Leu	487
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Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Pro Ser His 35 40 45	
Pro Met Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu 50 55 60	
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr 65 70 75 80	
Val Val Phe Ile Met Val Pro Phe Ser Met Ile Val Thr Ser Tyr Ile 85 90 95	
Arg Ile Leu Gly Ala Ile Leu Ala Met Thr Ser Thr Gln Ser Arg His 100 105 110	
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Cys Leu Phe 115 120 125	
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser 130 135 140	

Met Leu

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gtc t Val (tgt Cys	gcc Ala	cta Leu 20	atc Ile	ctc Leu	gtg Val	ttg Leu	tgc Cys 25	tgg Trp	gtc Val	ctc Leu	acc Thr	aac Asn 30	gtt Val	gtt Val		97
gcc t Ala l	ttg Leu	acc Thr 35	cac His	aca Thr	ctc Leu	ctc Leu	atg Met 40	gct Ala	cga Arg	ctg Leu	tcc Ser	ttc Phe 45	tgt Cys	gtg Val	act Thr		145
gly (gaa Glu 50	att Ile	gct Ala	cac His	ttt Phe	ttc Phe 55	tgt Cys	gac Asp	atc Ile	act Thr	cct Pro 60	gtc Val	ctg Leu	aag Lys	cta Leu		193
tca Ser 65	tgt Cys	tct Ser	gac Asp	acc Thr	cac His 70	atc Ile	aat Asn	gag Glu	atg Met	atg Met 75	gtt Val	ttt Phe	gtc Val	ttg Leu	gga Gly 80		241
ggc Gly	aca Thr	gta Val	ctc Leu	atc Ile 85	atc Ile	ccc Pro	ttt Phe	cta Leu	tgc Cys 90	att Ile	gtc Val	acc Thr	tcc Ser	tac Tyr 95	atc Ile		289
tac Tyr	att Ile	gtg Val	cct Pro 100	gct Ala	att Ile	ctg Leu	agg Arg	gtc Val 105	cga Arg	acc Thr	cat His	ggt Gly	999 Gly 110	gcg Ala	ggc Gly		337
aag Lys	Āla	Phe	tcc Ser	Thr	Cys	Ser	Ser	His	Leu	Cys	Ile	Val	tgt Cys	gtg Val	ttc Phe		385
tat Tyr	ggg Gly 130	Thr	ctc Leu	ttc Phe	agt Ser	gcc Ala 135	Tyr	ctg Leu	tgt Cys	cct Pro	ccc Pro 140	Ser	atc Ile	gcc Ala	tct Ser		433
gaa Glu 145	gat Asp	aag Lys	gac Asp	att Ile	gca Ala 150	Thr	gct Ala	gca Ala	atg Met	tat Tyr 155	Thr	ata Ile	gtg Val	act Thr	ccc Pro 160		481
-	ttg Leu																487

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Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
                     70
Gly Thr Val Leu Ile Ile Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
Tyr Ile Val Pro Ala Ile Leu Arg Val Arg Thr His Gly Gly Ala Gly
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Val Phe
Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
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 Glu Asp Lys Asp Ile Ala Thr Ala Ala Met Tyr Thr Ile Val Thr Pro
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 Thr Leu
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                                      10
                                                                      97
gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg
Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
                                25
gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa
                                                                     145
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
                            40
aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc
                                                                     1.93
Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
                        5.5
tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg
                                                                      241
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Phe Ile Val
65
gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt
                                                                      289
Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
                                    90
ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct
                                                                      337
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
             100
aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc
                                                                      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
                             120
ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc
                                                                      433
 Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
                         135
     130
 ctg gac cag ggg aaa gtg tet tee att ttt tat act gea gtg gtg eea
                                                                      481
 Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
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 145
                                                                      486
 tgt tt
 Cys
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Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val
Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
                                    90
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
            100
                                105
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
                            120
        115
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
Cys
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308

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49

97

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tac tgt gga cag ctg gtg gct ttc tct tac atg agt ggt ttc atg atc

Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile

Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly

20 25 30

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tct gtc atc Ser Val Ile 35	aag gtc Lys Val	tat ttc at Tyr Phe Il 40	t tca ca e Ser Hi	t gtt gct s Val Ala	t ttc tgt a Phe Cys 45	ggc tcc Gly Ser	145
aat gtt atg Asn Val Met 50	aac ctc Asn Leu	ttt ttc tg Phe Phe Cy 55	t gat at s Asp Il	c tca cca e Ser Pro	a gtc cta o Val Leu	aaa ctg Lys Leu	193
gca tgc aaa Ala Cys Lys 65	gac atg Asp Met	tcc aca gc Ser Thr Al 70	t gag ct a Glu Le	a gtg gad eu Val Asp 75	c ttt gct p Phe Ala	tta gct Leu Ala 80	241
atc gtc att Ile Val Ile	ctt gtg Leu Val 85	atc cct ct Ile Pro Le	c att ac u Ile Th 90	nr Thr Ile	c ctc tcc e Leu Ser	tat ato Tyr Ile 95	289
tac att gtc Tyr Ile Val	tcc gcc Ser Ala 100	att ctg ca Ile Leu Hi	t ata co s Ile Pr 105	cc tcc ac ro Ser Th	c cag gga r Gln Gly 110	Arg Lys	337
aag gcc ttc Lys Ala Phe 115	Ser Thr	tgt gca to Cys Ala Se 12	r His Le	tc act gt eu Thr Va	a gtc ata l Val Ile 125	att ttt E Ile Phe	385
tac aca gcc Tyr Thr Ala 130	atg att Met Ile	ttt aca ta Phe Thr Ty 135	at gtt co vr Val Ai	gg ccc ag rg Pro Ar 14	g Ala Ile	gca tca Ala Se:	a 433
ttt aat tcc Phe Asn Ser 145	aac aaa Asn Lys	cta atc to Leu Ile Se 150	ca gct g er Ala Va	tc tat gc al Tyr Al 155	a gtc cto a Val Let	aca cce I Thr Pro 16	2
atg cta Met Leu							487
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Tyr Cys Gl	y Gln Leu 20	ı Val Ala P	he Ser I 25	Tyr Met S	er Gly Ph 30	e Met Il	е
Ser Val I1 35			le Ser H O	His Val A	la Phe Cy 45	rs Gly Se	er

Asn Val Met Asn Leu Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu 50 55

Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala 75 Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys 105 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser 130 Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro 150 145 Met Leu <210> 363 <211> 488 <212> DNA <213> Saimiri boliviensis <220> <221> misc_feature (1)..(488) <222> <223> Taxon = 27679; gene = SBO220; pseudogene; Accession DDBJ/EMBL/GenBank = AF179840 <400> 363 tgtggccatc tgtaagcccc tgcattacac caccatcatg agcagcaaaa tctgcctgca 60 gettgtgett gggtgetggg ttettggttt teteateate ttteeaecae teetettagg 120 actaaatctt gacttctgtg cctccaacgt cgttgatcat ttctactgtg acactatccc 180 240 gctcctgcag atttcctgca cagacacgca gctcctggag aggatgggat tcatctcagc gctggtgaca ctcttagtca cattggtaat ggtgataata tcatatactt atattgccct 300 gacaattcta aaaatccctt caactagtca gaggaaaaag gctttttcca cgtgttcttc 360 tcacatgatt gtgatatccc tttcttatgg cagctgccat cttcatgtat gttaagccat 420 cagtcaaaca aagggtatct ttttcaaagg gaatttcggt gctcaatacc tctgttgctc 480 488 cacttttg

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                                                                       97
ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
gcc atg ttg cac act tta ctc ata gcc agg ttg cgt ttt tgt gca gac
                                                                      145
Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp
                            40
aat gtg atc ttc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
                                                                      193
Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
                                                                      241
gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
                                        75
                                                                      289
ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
                                    90
                                                                      337
cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc
Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
            100
aag gcc gtc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc
                                                                      385
Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
                             120
        115
tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct
                                                                      433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
                         135
act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc
                                                                      481
Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
                                         155
                     150
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Met Leu
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Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His

Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp

Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 105

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser 135 140 130

Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro 155 150

Met Leu

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gtg tgt ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg

97

<211> 487

Val Cys Leu	Leu Leu Leu 20	Leu Gly Val 25	Tyr Gly Met	Gly Val Leu 30	Gly
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			atc ctt ccc Ile Leu Pro 60		
			ctg gtc atc Leu Val Ile 75		
acc att ggc Thr Ile Gly	att ggg gtg Ile Gly Val 85	ccc att gtt Pro Ile Val	gcc att ttt Ala Ile Phe 90	atc tct tat Ile Ser Tyr 95	ggt 289 Gly
	_		agt tct gct Ser Ser Ala		
aaa gcc ttc Lys Ala Phe 115	Ser Thr Cys	agc tcc cac Ser Ser His 120	ata att gca Ile Ile Ala	gtt tct ctt Val Ser Leu 125	ttc 385 Phe
ttc ggg tca Phe Gly Ser 130	gga gct ttt Gly Ala Phe	atg tac ctc Met Tyr Leu 135	aaa ccc tct Lys Pro Ser 140	tcc gtt tta Ser Val Leu	ccc 433 Pro
ctg gac cag Leu Asp Glr 145	ggg aaa gta Gly Lys Val 150	. Ser Ser Leu	ttt tat act Phe Tyr Thr 155	att gtg gtg Ile Val Val	ccc 481 Pro 160
atg ttt Met Phe					487
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Val Cys Let	ı Leu Leu Leı 20	ı Leu Gly Val 25	l Tyr Gly Met	Gly Val Let 30	Gly
Ala Val Ala 35	a His Thr Gl	y Asn Ile Vai 40	l Phe Leu Thr	Phe Cys Ala 45	Gly
Asn Leu Va	l Asn His Ty	r Met Cys As _] 55	p Ile Leu Pro 60	Leu Leu Glı	ı Leu

Ser 65	Cys	Asn	Gly	Ser	Tyr 70	Ile	Asn	Val	Leu	Val 75	Ile	Phe	Ile	Val	Va⊥ 80	
Thr	Ile	Gly	Ile	Gly 85	Val	Pro	Ile	Val	Ala 90	Ile	Phe	Ile	Ser	Tyr 95	Gly	
Phe	Ile	Leu	Ser 100	Ser	Asn	Leu	His	Ile 105	Ser	Ser	Ala	Glu	Gly 110	Arg	Ser	
Lys	Ala	Phe 115	Ser	Thr	Cys	Ser	Ser 120	His	Ile	Ile	Ala	Val 125	Ser	Leu	Phe	
Phe	Gly 130	Ser	Gly	Ala	Phe	Met 135	Tyr	Leu	Lys	Pro	Ser 140	Ser	Val	Leu	Pro	
Leu 145	Asp	Gln	Gly	Lys	Val 150	Ser	Ser	Leu	Phe	Tyr 155	Thr	Ile	Val	Val	Pro 160	
Met	Phe															
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t g	00> gtg g Val 1	368 gcc Ala	atc Ile	Cys I	cac (His !	ccc (Pro 1	ctg (Leu I	cac ' His '	lyr	aca q Thr '	gtc : Val '	acc (att Ile	ASII	ccc ag Pro Ar 15	ra 49 rg
ct: Le	g tg ı Cy	t gg s Gl	a ct y Le 20	u Lei	g gt ı Va	t cte	g gca	a tc a Se 25	c tg r Tr	g at p Il	c ct e Le	g ag u Se	t gc r Al 30	c ct a Le	g aat u Asn	97
tc Se	c tc r Se	a tt r Le 35	u Gl	a acon n Th	c tt r Le	a at u Il	a gt e Va 40	g ct l Le	g cg u Ar	g ct g Le	t tc u Se	c tt r Ph 45	e cy	c ac s Th	a gac r Asp	145
tt Le	g ga u Gl 50	u Il	c cc e Pr	c ca o Hi	c tt s Ph	t tt e Ph 55	е Су	c ga s Gl	a ct u Le	t aa u As	t ca n Gl 60	n va	c at	a ca e Hi	t ctt s Leu	193
gc Al 65	а Су	t ta s Ty	it ga r As	ıc ac sp Th	t tt r Ph 70	e Le	t aa u As	t ga n As	t gt p Va	g gt il Va 75	T Me	g ta et Ty	ıt tt r Le	g go eu Al	a gct a Ala 80	241

atg ctg ctg ggc ggt ggt ccc ctc aca gga att att tac tct tac tct Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser 85 90 95	289
aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr 100 105 110	337
aag gcg ttt tcc acc tgt gca tct cac atc tta att gtc tcc tta ttt Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe 115 120 125	385
tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gca act ggc aac Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 130 135 140	433
tca cat tca agt gct gca gcc ttg gtg atg tac act gtg gtc acc ccc Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro 145 150 155 160	481
atg ctg Met Leu	487
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Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn

Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro 155

Met Leu

<210> 370 <211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

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cag ata ttt ttc ttc att gtg ttt gga tgc ctg gac aat tta ctc cta 145 Gln Ile Phe Phe Phe Ile Val Phe Gly Cys Leu Asp Asn Leu Leu 35

tca gtg atg gcc tat gac cgc ttt gtg gcc atc tgc cat ccc ttg cac 193 Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55

tat gtg gtc atc atg aat tct tgc ttc tgt gtg atg ctg gct ctt gga 241 Tyr Val Val Ile Met Asn Ser Cys Phe Cys Val Met Leu Ala Leu Gly

tca tgg ata gtc agc gtc atg agt tcc cta cct gag acc ttg act gtg 289 Ser Trp Ile Val Ser Val Met Ser Ser Leu Pro Glu Thr Leu Thr Val 85

tta aga cta tcc ttc tgt aca aac atg gaa att cca cac ttt ttc tgt 337 Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys 105

gat ctt ccc gaa gtc ctg aag ctt gcc tgt tct gac acc ctt gtt aat 385 Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Leu Val Asn 115

aac att gtg aca tat tct ata acc ata gtc ata gct ggt ttc cca ttc

Asn	Ile 130	Val	Thr	Tyr	Ser	Ile 135	Thr	Ile	Val	Ile	Ala 140	Gly	Phe	Pro	Phe	
tct Ser 145	G1À 333	att Ile	cta Leu	ttg Leu	tct Ser 150	tat Tyr	tct Ser	aag Lys	att Ile	ttc Phe 155	tcc Ser	tcc Ser	atc Ile	cta Leu	aga Arg 160	481
att Ile	cct Pro	tca Ser	gct Ala	999 Gly 165	ggc Gly	aag Lys	tac Tyr	aaa Lys	gcc Ala 170	ttt Phe	tct Ser	acc Thr	tgt Cys	999 Gly 175	tct Ser	529
cat His	ctt Leu	ttg Leu	gtg Val 180	gtc Val	ttc Phe	tta Leu	ttc Phe	tat Tyr 185	agc Ser	aat Asn	ggt Gly	ctt Leu	999 Gly 190	gtc Val	tac Tyr	577
	agc Ser															625
_	atg Met 210		_		_											649
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AF'0	73959	9														
<40		9 371														
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<400 Ile 1	0 > 3	371 Asp		5					10					15		
<400 Ile 1 Thr	0> 3 Ala	Asp	Thr 20	5 Gln	Ser	Lys	Phe	Ile 25	10 Ser	Phe	Ser	Gly	Cys 30	15	Thr	
<400 Ile 1 Thr	0> 3 Ala Ile	Asp His Phe	Thr 20	Gln Phe	Ser	Lys Val	Phe Phe 40	Ile 25 Gly	10 Ser Cys	Phe Leu	Ser Asp	Gly Asn 45	Cys 30 Leu	15 Ile Leu	Thr Leu	
<400 Ile 1 Thr Gln	O> 3 Ala Ile Ile Val	Asp His Phe 35	Thr 20 Phe	Gln Phe Tyr	Ser Ile Asp	Lys Val Arg 55	Phe Phe 40	Ile 25 Gly Val	10 Ser Cys Ala	Phe Leu Ile	Ser Asp Cys 60	Gly Asn 45	Cys 30 Leu Pro	Ile Leu Leu	Thr Leu His	
<400 Ile 1 Thr Gln Ser	O> 3 Ala Ile Ile Val	Asp His Phe 35 Met	Thr 20 Phe Ala Ile	Gln Phe Tyr Met	Ser Ile Asp Asn 70	Lys Val Arg 55	Phe Phe 40 Phe Cys	Ile 25 Gly Val	Ser Cys Ala	Phe Leu Ile Val 75	Ser Asp Cys 60 Met	Gly Asn 45 His	Cys 30 Leu Pro	Ile Leu Leu	Thr Leu His Gly 80	
<400 Ile 1 Thr Gln Ser Tyr 65	O> 3 Ala Ile Ile Val 50 Val	Asp His Phe 35 Met Val	Thr 20 Phe Ala Ile Val	Gln Phe Tyr Met Ser 85	Ser Ile Asp Asn 70 Val	Lys Val Arg 55 Ser	Phe Phe 40 Phe Cys	Ile 25 Gly Val Phe	Ser Cys Ala Cys Leu	Phe Leu Ile Val 75	Ser Asp Cys 60 Met	Gly Asn 45 His	Cys 30 Leu Pro Ala	Ile Leu Leu Thr	Thr Leu His Gly 80 Val	

115 120 125

Asn Ile Val Thr Tyr Ser Ile Thr Ile Val Ile Ala Gly Phe Pro Phe 135 Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile Phe Ser Ser Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175 His Leu Leu Val Val Phe Leu Phe Tyr Ser Asn Gly Leu Gly Val Tyr 180 185 190 Leu Ser Ser Ala Ala Thr Ser Ser Ser Arg Met Ser Leu Val Ala Ser 195 200 205 Leu Met Tyr Ser Ile Val Thr Pro 210 215 <210> 372 <211> 649 <212> DNA <213> Mus musculus domesticus <220> <221> misc_feature
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<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 372 c ttc tct gac ttc tgc ttt tcc tct gtg acc att ccc aaa ttg ctg cag Phe Ser Asp Phe Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln 49 10 off doe for ata occ tat doe got too otg goa 97 5

	_		_		gtt Val						-		_	-	-	97
	_				ctg Leu			_	_			_				145
	_	_	_		gat Asp	_			_		_					193
		_		_	agc Ser 70		_	_	_		_	_	~ ~	-		241
tct	tgg	cta	ctg	acc	aca	gtc	atc	tct	ttg	tca	cac	aca	ctg	ctc	atg	289

Ser	Trp	Leu	Leu	Thr 85	Thr	Val	Ile	Ser	Leu 90	Ser	His	Thr	Leu	Leu 95	Met	
gct Ala	cgg Arg	ctc Leu	tcc Ser 100	ttc Phe	tgt Cys	gct Ala	aac Asn	aat Asn 105	gtg Val	att Ile	cct Pro	cac His	ttt Phe 110	ttc Phe	tgt Cys	337
											gac Asp					385
											att Ile 140					433
											tcc Ser					481
											tcc Ser					529
											atc Ile					577
											gag Glu					625
	atg Met 210															649
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< 40	0 > 3	373														
Phe 1	Ser	Asp	Phe	Cys 5	Phe	Ser	Ser	Val	Thr 10	Ile	Pro	Lys	Leu	Leu 15	Gln	
Asn	Met	Gln	Ser 20	Gln	Val	Pro	Ser	Ile 25	Pro	Tyr	Ala	Gly	Cys 30	Leu	Ala	
Gln	Met	Tyr 35	Phe	Phe	Leu	Leu	Phe 40	Ala	Asp	Leu	Glu	Ser 45	Phe	Leu	Leu	
Val	Ala 50	Met	Ala	Tyr	Asp	Arg 55	Tyr	Val	Ala	Ile	Cys 60	Phe	Pro	Leu	His	
Tyr	Thr	Ser	Ile	Met	Ser	Pro	Lys	Leu	Cys	Leu	Cys	Leu	Val	Ala	Leu	

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Ser Trp Leu Leu Thr Thr Val Ile Ser Leu Ser His Thr Leu Leu Met

Ala Arg Leu Ser Phe Cys Ala Asn Val Ile Pro His Phe Phe Cys

Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Gln Ile Asn 120

Lys Leu Met Ile Phe Ile Leu Gly Gly Leu Val Ile Ile Val Pro Phe 130 135

Leu Leu Ile Phe Ser Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 150

Val Pro Ser Ser Arg Ser Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr

Leu Arg Pro Ser Ala Asn Asn Ser Thr Ile Lys Glu Thr Val Met Ala 200

Val Met Tyr Thr Val Val Thr Pro

<210> 374

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)
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<221> CDS

<222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 374

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97 aac atg cag agc cag gac tca tcc atc acc tat gca gga tgc ctg aca Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr 25

caa atg tac ttt ttc ttg ctc ttt gga gac ctt gag agc ttc ctc ctt 145 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu

		35					40					45					
													ccc Pro			:	193
													gtg Val			:	241
			_					-	_	_			ctg Leu		_		289
-	_	_			-		_			_			ttt Phe 110	_			337
-	_		_	_	_	_	_		_		_		cac His				385
													att Ile				433
													att Ile				481
gtc Val	ccg Pro	tct Ser	gct Ala	cga Arg 165	ggc Gly	atc Ile	cgt Arg	aaa Lys	gcc Ala 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	999 Gly 175	tcc Ser		529
													ggt Gly 190				577
tta Leu	tgt Cys	cca Pro 195	tca Ser	gct Ala	gat Asp	aac Asn	tct Ser 200	act Thr	gtg Val	aag Lys	gaa Glu	act Thr 205	gtc Val	atg Met	gcc Ala		625
_	_	Tyr		gtg Val													649
<21 <21 <21 <21	1> 2>	375 216 PRT Mus	musc	ulus	dom	esti	cus										
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Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr 20 25 30

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Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
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Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
```

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn 115

Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe 135

Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 155 150

Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 165 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr 180

Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala

Met Met Tyr Thr Val Val Thr Pro 210

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<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

(1)..(649)

<223> Taxon = 10092; clone = OR11M; Accession DDBJ/EMBL/GenBank = AF073962

<220>

<221> CDS <222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains

<400> 376

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aat atg cag agc cag gac cca tcc atc ccc tat gga ggt tgc ctg gca Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala 20 25 30	97
caa ata ttc ttc ttt atg ctt ttt gga gac atg gaa agc ttc ctt ctt Gln Ile Phe Phe Met Leu Phe Gly Asp Met Glu Ser Phe Leu Leu 35 40 45	145
gta gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60	193
tac act agc atc atg agt cct aag gtc tgt act ttt cta gtg cta ctg Tyr Thr Ser Ile Met Ser Pro Lys Val Cys Thr Phe Leu Val Leu Leu 65 70 75 80	241
ttg tgg ata ctg aca aca cca cat gcc aca atg caa att ctg ctc aca Leu Trp Ile Leu Thr Thr Pro His Ala Thr Met Gln Ile Leu Leu Thr 85 90 95	289
gta aga ctg tct ttt tgt gag aac aat gtg ttt ctc aac ttt ttc tgt Val Arg Leu Ser Phe Cys Glu Asn Asn Val Phe Leu Asn Phe Phe Cys 100 105 110	337
gac ata ttt gtt ctc tta aag ctg gcc tgc tca gac act tat gtt aat Asp Ile Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 115 120 125	385
gat ttg atg ata ctt atc atg gga ggg ctc atc att gtt att cca ttc Asp Leu Met Ile Leu Ile Met Gly Gly Leu Ile Ile Val Ile Pro Phe 130 135 140	433
ctg ctc att gtt ata tcc tat gca agg atc atc tcc tct act ctt aag Leu Leu Ile Val Ile Ser Tyr Ala Arg Ile Ile Ser Ser Thr Leu Lys 145 150 150	481
gtt cca tct act caa ggc atc cac aag gtc ttc tct acc tgt ggc tct Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	529
cat ctg tct gtg gtg tct ctg ttc tat ggg aca att att ggt ctc tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	577
tta tgt cca tca ggt aat aat ttc agt cta aag ggg tct gcc atg gct Leu Cys Pro Ser Gly Asn Asn Phe Ser Leu Lys Gly Ser Ala Met Ala 195 200 205	625
atg atg tac aca gtg gtg act ccc Met Met Tyr Thr Val Val Thr Pro 210 215	649
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Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala

Gln Ile Phe Phe Phe Met Leu Phe Gly Asp Met Glu Ser Phe Leu Leu 40

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Val Cys Thr Phe Leu Val Leu Leu

Leu Trp Ile Leu Thr Thr Pro His Ala Thr Met Gln Ile Leu Leu Thr

Val Arg Leu Ser Phe Cys Glu Asn Asn Val Phe Leu Asn Phe Phe Cys 105

Asp Ile Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 120

Asp Leu Met Ile Leu Ile Met Gly Gly Leu Ile Ile Val Ile Pro Phe 130

Leu Leu Ile Val Ile Ser Tyr Ala Arg Ile Ile Ser Ser Thr Leu Lys 145

Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr

Leu Cys Pro Ser Gly Asn Asn Phe Ser Leu Lys Gly Ser Ala Met Ala 200 195

Met Met Tyr Thr Val Val Thr Pro 215

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	c to									r Me					a cag u Gln	49
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caa Gln	atg Met	tac Tyr 35	ttt Phe	tta Leu	ttg Leu	gtt Val	ttt Phe 40	gga Gly	gac Asp	ctg Leu	gag Glu	agc Ser 45	atc Ile	ctt Leu	ctt Leu	145
ttg Leu	gtc Val 50	atg Met	gct Ala	tat Tyr	gac Asp	cgg Arg 55	tat Tyr	gtg Val	gct Ala	gtc Val	tgc Cys 60	ttc Phe	ccc Pro	ctt Leu	cat His	193
tac Tyr 65	atg Met	agc Ser	atc Ile	atg Met	agc Ser 70	ccc Pro	aca Thr	ctc Leu	tgt Cys	gtg Val 75	tgt Cys	ctg Leu	cta Leu	gtg Val	tta Leu 80	241
tcc Ser	tgg Trp	gta Val	ttt Phe	act Thr 85	gtg Val	ctg Leu	tat Tyr	tct Ser	atg Met 90	ttg Leu	cac His	act Thr	cta Leu	ctc Leu 95	ttg Leu	289
tct Ser	aga Arg	ttg Leu	tca Ser 100	ttc Phe	tgt Cys	gag Glu	gat Asp	aac Asn 105	ttg Leu	atc Ile	cac His	cac His	ttt Phe 110	ttc Phe	tgt Cys	337
gac Asp	ata Ile	tct Ser 115	gcc Ala	ctg Leu	ctc Leu	aag Lys	ttg Leu 120	gct Ala	tgc Cys	tct Ser	gac Asp	att Ile 125	cat His	att Ile	aat Asn	385
gaa Glu	tta Leu 130	atg Met	ata Ile	ttt Phe	atc Ile	atg Met 135	gga Gly	Gly aaa	ctt Leu	gtt Val	agc Ser 140	atc Ile	atc Ile	cca Pro	ttc Phe	433
tta Leu 145	ctc Leu	att Ile	gtt Val	gtg Val	tcc Ser 150	Tyr	ata Ile	caa Gln	att Ile	gtc Val 155	tac Tyr	tcc Ser	att Ile	cta Leu	aag Lys 160	481
att Ile	tca Ser	tct Ser	gct Ala	cat His 165	gtt Val	tta Leu	cac His	aag Lys	atc Ile 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	999 Gly 175	Ser	529
cac His	ctg Leu	tct Ser	gta Val 180	Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly	aca Thr	att Ile	ttt Phe	gct Ala 190	ctc Leu	tac Tyr	577
tta Leu	tgt Cys	cca Pro 195	Ser	gct Ala	aat Asn	aac Asn	tct Ser 200	Thr	gtg Val	aag Lys	gag Glu	att Ile 205	Ser	atg Met	gcc Ala	625
		Cys				act Thr 215	Pro									649

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- <213> Mus musculus domesticus
- <220>
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<400> 379

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Gln Met Tyr Phe Leu Leu Val Phe Gly Asp Leu Glu Ser Ile Leu Leu

Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Phe Pro Leu His 55

Tyr Met Ser Ile Met Ser Pro Thr Leu Cys Val Cys Leu Leu Val Leu 70

Ser Trp Val Phe Thr Val Leu Tyr Ser Met Leu His Thr Leu Leu 90

Ser Arg Leu Ser Phe Cys Glu Asp Asn Leu Ile His His Phe Phe Cys 105

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn

Glu Leu Met Ile Phe Ile Met Gly Gly Leu Val Ser Ile Ile Pro Phe

Leu Leu Ile Val Val Ser Tyr Ile Gln Ile Val Tyr Ser Ile Leu Lys

Ile Ser Ser Ala His Val Leu His Lys Ile Phe Ser Thr Cys Gly Ser

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Phe Ala Leu Tyr

Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Ile Ser Met Ala 200

Met Met Cys Thr Val Val Thr Pro

<210 <211 <212 <213 <220 <221 <222	> 6 > D > M > m	49 NA us m isc_ 1)	feat [.]	ure	dome	stic	us										
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<400 c tt Ph 1	t to	80 t ga r As	c at p Il	t gg e Gl 5	rt tt y Ph	c at le Il	c to e Se	t ac er Th	a ac ir Th	ır Il	c cc e Pr	t aa o Ly	ıg at rs Me	g tt t Le 15	g gtg u Val	49	
aat Asn	atc Ile	caa Gln	aca Thr 20	cag Gln	agc Ser	aag Lys	tcc Ser	atc Ile 25	tcc Ser	tat Tyr	gca Ala	gaa Glu	tgc Cys 30	atc Ile	acc Thr	97	
cag Gln	att Ile	tat Tyr 35	ttt Phe	ttc Phe	atg Met	ctc Leu	ttt Phe 40	gga Gly	ggc Gly	atg Met	gac Asp	ata Ile 45	ctt Leu	ctc Leu	ctc Leu	145	
acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctt Leu	cac His	193	
tat Tyr 65	tca Ser	gtc Val	att Ile	atg Met	aat Asn 70	ccc Pro	caa Gln	cta Leu	agt Ser	ggc Gly 75	ttg Leu	ctg Leu	gtt Val	ctt Leu	gta Val 80	241	
tca Ser	tgg Trp	ttt Phe	att Ile	agc Ser 85	ttt Phe	tca Ser	tat Tyr	tct Ser	ctg Leu 90	ata Ile	cag Gln	agt Ser	cta Leu	ttg Leu 95	atg Met	289	
ctg Leu	cgg Arg	ttg Leu	tcc Ser 100	ttc Phe	tgt Cys	aca Thr	aat Asn	cag Gln 105	ata Ile	att Ile	aaa Lys	cac His	ttt Phe 110	tac Tyr	tgt Cys	337	
gaa Glu	tat Tyr	tct Ser 115	aga Arg	gcc Ala	ctc Leu	Thr	ata Ile 120	Ala	Cys	Ser	gac Asp	Thr	Leu	atc Ile	aat Asn	385	
cat His	atc Ile 130	ctt Leu	ctt Leu	tat Tyr	att Ile	ctg Leu 135	ata Ile	tgt Cys	gtc Val	ctt Leu	ggc Gly 140	ttc Phe	atc Ile	cct Pro	ttc Phe	433	
tca Ser 145	gly ggg	atc Ile	ctt Leu	tat Tyr	tca Ser 150	tac Tyr	tgt Cys	aaa Lys	att Ile	gtt Val 155	tct Ser	tct Ser	att Ile	ttg Leu	aga Arg 160	481	
att Ile	cca Pro	tca Ser	aca Thr	gat Asp 165	gga Gly	aaa Lys	tat Tyr	aaa Lys	gca Ala 170	Phe	tct Ser	acc Thr	tgt Cys	999 Gly 175	tct Ser	529	
cat	cta	tca	gtg	gtt	tct	tta	ttc	tat	999	aca	ggc	ctt	ggt	gtg	tac	577	

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 ctt agt tct gat gta act tcc tcc tct ggg aag gac gtg gtg gcc tca 625 Leu Ser Ser Asp Val Thr Ser Ser Gly Lys Asp Val Val Ala Ser 200 649 gta atg tat aca gtg gtc acc cct Val Met Tyr Thr Val Val Thr Pro <210> 381 <211> 216 <212> PRT <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649)
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His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 185

Leu Ser Ser Asp Val Thr Ser Ser Gly Lys Asp Val Val Ala Ser

Val Met Tyr Thr Val Val Thr Pro

<210> 382 <211> 643 <212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(643)

<223> Taxon = 10092; clone = OR15-71M20; Accession DDBJ/EMBL/GenBank = AF073965

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<221> CDS

<222> (2)..(643) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 382

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97 gac ctc cta tcg gcg aag aaa acc atc tca ata gaa ggc tgc ctg gct Asp Leu Leu Ser Ala Lys Lys Thr Ile Ser Ile Glu Gly Cys Leu Ala 20 25

145 cag gtc ttt ttt gtg ttt ttt cct tct ggt act gaa gcc tgc ctg ctc Gln Val Phe Phe Val Phe Phe Pro Ser Gly Thr Glu Ala Cys Leu Leu 35 40

tct gtc atg gct tat gac cgc tat gct gcc atc tgc cat ccc ctg ctc 193 Ser Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu 50

241 tac qqc caq qtq atq aga aat gag ttg tgt gta agg ctt gtg gtc atc Tyr Gly Gln Val Met Arg Asn Glu Leu Cys Val Arg Leu Val Val Ile 75

tca tgg ggc gtg gcc tct ctc aac gca acc atc atc gtg ctc ttg gct 289 Ser Trp Gly Val Ala Ser Leu Asn Ala Thr Ile Ile Val Leu Leu Ala 90

gtc aac ctg gac ttc tgt ggg gct caa acc att cac cac tac acc tgt 337 Val Asn Leu Asp Phe Cys Gly Ala Gln Thr Ile His His Tyr Thr Cys 100

gag ctg cct gcc ctt ttc ccc ttg tcc tgt tcc gat atc tcc atc act 385 Glu Leu Pro Ala Leu Phe Pro Leu Ser Cys Ser Asp Ile Ser Ile Thr 120 115

gtc gtc gtc ctg ctt tgc tcc agc ttg ctg cat ggg ctg gga acc ttt 433

Val Val V 130	Val Leu	Leu	Cys	Ser 135	Ser	Leu	Leu	His	Gly 140	Leu	Gly	Thr	Phe	
atc cct a Ile Pro I 145					_	_		_		_		_	_	481
atc agt t Ile Ser S														529
cac ctc o		Val												577
ctc atg (Leu Met 1														625
tac agc of Tyr Ser 2														643
<211> 2 <212> P	83 14 RT us musc	ulus	dome	estio	cus									
<222> (isc_fea	3)	•		0.7							- /		1e _
AF073965		1009.	2; C	Lone	= 01	R15-	71M2	O; A	ccess	sion	DDB	J∕EMI	BL/GenBan	к =
AF073965		1009.	2; C1	lone	= 01	R15-	71M2	O; A	cces	sion	DDB	J / EMI	BL/GenBan	к =
AF073965	83													K =
AF073965 <400> 3 Phe Val	83 Asp Lei	ı Cys 5	Phe	Ser	Ser	Val	Thr 10	Val	Pro	Lys	Leu	Leu 15	Lys	к =
AF073965 <400> 3 Phe Val 1 Asp Leu Gln Val	83 Asp Let Leu Se: 20	ı Cys 5	Phe Lys	Ser Lys	Ser	Val Ile 25	Thr 10 Ser	Val	Pro	Lys	Leu Cys 30	Leu 15 Leu	Lys Ala	к =
AF073965 <400> 3 Phe Val 1 Asp Leu Gln Val	83 Asp Let Let Se: 20 Phe Pho	Cys 5 Ala Val	Phe Lys Phe	Ser Lys Phe	Ser Thr Pro	Val Ile 25 Ser	Thr 10 Ser	Val Ile Thr	Pro Glu Glu	Lys Gly Ala 45	Leu Cys 30 Cys	Leu 15 Leu Leu	Lys Ala Leu	к =
AF073965 <400> 3 Phe Val 1 Asp Leu Gln Val Ser Val	Asp Let Se: 20 Phe Pho 35 Met Ala	Cys 5 Ala Val	Phe Lys Phe Asp	Ser Lys Phe Arg	Ser Thr Pro 40 Tyr	Val Ile 25 Ser	Thr 10 Ser Gly	Val Ile Thr	Pro Glu Glu Cys	Lys Gly Ala 45	Leu Cys 30 Cys	Leu 15 Leu Leu	Lys Ala Leu Leu	к =
AF073965 <400> 3 Phe Val 1 Asp Leu Gln Val Ser Val 50 Tyr Gly	Asp Let Let Se: 20 Phe Phe 35 Met Ala Gln Val	Cys 5 Ala Val Tyr	Phe Lys Phe Asp	Ser Lys Phe Arg 55 Asn	Ser Thr Pro 40 Tyr	Val Ile 25 Ser Ala	Thr 10 Ser Gly Ala Cys	Val Ile Thr Ile Val 75	Pro Glu Glu Cys 60	Lys Gly Ala 45 His	Leu Cys 30 Cys Pro	Leu 15 Leu Leu Val	Lys Ala Leu Leu Ile 80	к =
AF073965 <400> 3 Phe Val 1 Asp Leu Gln Val Ser Val 50 Tyr Gly 65	Asp Let Se: 20 Phe Pho 35 Met Ala Gln Va	Cys 5 Ala Val ATyr Ala Ala 85	Phe Lys Phe Asp Arg 70 Ser	Ser Lys Phe Arg 55 Asn Leu	Ser Thr Pro 40 Tyr Glu Asn	Val Ile 25 Ser Ala Leu Ala	Thr 10 Ser Gly Ala Cys Thr 90	Val Ile Thr Ile Val 75	Pro Glu Glu Cys 60 Arg	Lys Gly Ala 45 His Leu Val	Leu Cys 30 Cys Pro Val	Leu 15 Leu Leu Val Leu 95	Lys Ala Leu Leu Ile 80 Ala	K =

Val Val Leu Leu Cys Ser Ser Leu Leu His Gly Leu Gly Thr Phe 135

Ile Pro Ile Phe Phe Ser Tyr Ala Arg Ile Val Ser Ala Ile Leu Ser

Ile Ser Ser Thr Thr Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser 170

His Leu Ala Ala Val Thr Leu Phe Phe Gly Ser Gly Phe Leu Cys Tyr 190 180 185

Leu Met Pro Pro Ser Gly Ser Ser Leu Asp Leu Leu Ser Leu Gln 200 205

Tyr Ser Ala Val Thr Pro

<210> 384

<211> 643

<212> DNA <213> Mus musculus domesticus

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<221> misc_feature

<222> (1)..(643)
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<221> CDS

<222> (2)..(643)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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97 aac cat ctc cta ggt agc aag gcc atc tcc ttt ggg gga tgt atg gca Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala 25

145 cag atg tac ttc atg ata tca ttg gga aac aca gac agt tat ata cta Gln Met Tyr Phe Met Ile Ser Leu Gly Asn Thr Asp Ser Tyr Ile Leu

gct gca atg gca tat gac cga gct gtg gct atc agt cgc ccg ctt cat 193 Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His 50

tat gca aca att atg agt cca caa ctt tgt gtc ctg ctg gtt gct ggg 241 Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly 80 70

tcc tgg gtg att gca aat gct aat gca ctg ccc cac acc cta ctc aca 289

56	er '	Trp	vai	iie	85	Asn	Ala	Asn	Ala	Leu 90	Pro	His	Thr	Leu	Leu 95	Thr	
g(ct la .	aga Arg	ttg Leu	tcc Ser 100	ttc Phe	tgt Cys	ggc Gly	aat Asn	aag Lys 105	gat Asp	gtg Val	gcc Ala	aac Asn	ttc Phe 110	tac Tyr	tgt Cys	337
_					_		_	_		_		gac Asp		_			385
	al :											tct Ser 140					433
C												aca Thr					481
												acc Thr					529
												atg Met					577
C:	gg rg	ccc Pro	ctg Leu 195	acc Thr	agt Ser	tac Tyr	agt Ser	ctg Leu 200	aag Lys	cat His	gca Ala	ttg Leu	ata Ile 205	act Thr	gtg Val	atg Met	625
	yr	_	_	gtg Val													643
<	210 211 212 213	.> 2 !> 1	385 214 PRT Mus 1	nusci	ulus	dome	esti	cus									
< <	220 221 222 223 F07	.> r	(1). Taxoı	_feat .(64) n = :	3)	2; c	lone	= O	R15-	71M2	1; A	cces	sion	DDB	J/EM	BL/GenBai	nk =
<	400)> :	385														
L 1		Val	Asp	Ile	Phe 5	Phe	Ser	Ser	Val	Thr 10	Ile	Pro	Lys	Met	Leu 15	Ala	
A	sn	His	Leu	Leu 20	Gly	Ser	Lys	Ala	Ile 25	Ser	Phe	Gly	Gly	Cys 30	Met	Ala	
G	ln	Met	Tyr 35	Phe	Met	Ile	Ser	Leu 40	Gly	Asn	Thr	Asp	Ser 45	Tyr	Ile	Leu	
А	la	Ala 50	Met	Ala	Tyr	Asp	Arg 55	Ala	Val	Ala	Ile	Ser 60	Arg	Pro	Leu	His	
Т	yr	Ala	Thr	Ile	Met	Ser	Pro	Gln	Leu	Cys	Val	Leu	Leu	Val	Ala	Gly	

Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr

Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys 105

Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn 115 120

Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu 135

Cys Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val

Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His

Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe 185

Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met 200

Tyr Thr Ala Val Thr Pro 210

<210> 386

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)
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<220>

<221> CDS

<222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 386

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aac ttg ctg aca cag aga aag aca atc ctc ttt gcc cag tgc ctc act Asn Leu Leu Thr Gln Arg Lys Thr Ile Leu Phe Ala Gln Cys Leu Thr 20

145 caa atg tat ttc ttt gtg gct ttt ggt att aca gac agt ttc ctt ttg

GIN	Met	Tyr 35	Phe	Phe	Val	Ala	Phe 40	Gly	Ile	Thr	Asp	Ser 45	Phe	Leu	Leu		
gct Ala	gcg Ala 50	atg Met	gcc Ala	att Ile	gac Asp	cgc Arg 55	tat Tyr	gtt Val	gct Ala	att Ile	tgc Cys 60	aat Asn	ccg Pro	ctt Leu	cat His		193
					agt Ser 70												241
					cat His										_		289
	_				tgt Cys				-						_		337
	_				ctg Leu				_		_						385
					aca Thr												433
_		_	_		ctt Leu 150								_	_			481
gtc Val	cct Pro	tca Ser	Gly aaa	gaa Glu 165	gga Gly	agg Arg	tac Tyr	aaa Lys	gtt Val 170	ttc Phe	tct Ser	acc Thr	tgt Cys	999 Gly 175	tct Ser		529
			_	_	gca Ala	_											577
					acc Thr												625
_				_	gtt Val												649
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<40	0> 3	387															
Leu 1	Val	Asp	Ile	Cys 5	Phe	Thr	Thr	Val	Ile 10	Val	Pro	Gln	Met	Leu 15	Val		

Asn Leu Leu Thr Gln Arg Lys Thr Ile Leu Phe Ala Gln Cys Leu Thr

Gln Met Tyr Phe Phe Val Ala Phe Gly Ile Thr Asp Ser Phe Leu Leu

Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu His

Tyr Asn Thr Val Met Ser Pro Arg Arg Cys Arg Leu Leu Val Val Ala 70

Ser Trp Ala Val Ser His Leu His Ser Leu Thr His Thr Ile Leu Met

Gly Arg Leu Ser Phe Cys Gly Pro Asn Val Ile His His Phe Phe Cys

Asp Val Gln Pro Leu Leu Thr Leu Ser Cys Ser Asp Thr Ser Ile Asn

Glu Leu Leu Ala Phe Thr Glu Gly Ser Val Val Ile Met Ser Pro Phe

Ile Leu Leu Ser Leu Ile Ser Ile Phe Thr Arg Thr Val Leu Arg 150

Val Pro Ser Gly Glu Gly Arg Tyr Lys Val Phe Ser Thr Cys Gly Ser

His Leu Thr Val Val Ala Leu Phe Tyr Gly Thr Ile Ile Ser Val Tyr

Ile Arg Pro Ser Ser Thr Tyr Ser Val Thr Lys Asp Arg Val Val Thr 195 200

Val Ile Tyr Thr Val Val Thr Pro 210

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<213> Mus musculus domesticus

<220>

<221> misc feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR18M; Accession DDBJ/EMBL/GenBank = AF073968

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<222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg aca Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr 20 25 30	97
caa atg tac ttt ttc agt gtt ttt gga agt ctg gag ata ttc ctt ctt Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45	145
gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt caa Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln 50 55 60	193
tat tcc agc atc atg agc ccc aat ctc tgt gtg tgt gtg gtg gtg ttc Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 65 70 75 80	241
tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc ttg Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu 85 90 95	289
gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc tgt Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110	337
gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att aat Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125	385
gaa tta atg ata ctt atc ttg gga ggg ttt ctt ctt gtc atc tca ctc Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135 140	433
tta ctc atc att gta tcc tat gta caa att gtc tcc tca att tta agg Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160	481
att tot tot act ogg got ato cat aag oto tto too aco tgt ggo toa Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175	529
cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt ctg tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	577
tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg tcc Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205	625
ctg atg tac aca gtg gtg act ccc Leu Met Tyr Thr Val Val Thr Pro 210 215	649
<210> 389 <211> 216 <212> PRT <213> Mus musculus domesticus	
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<222> (1)..(649)
<223> Taxon = 10092; clone = OR18M; Accession DDBJ/EMBL/GenBank = AF073968
<400> 389

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Gln 1 10 15

Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr 20 25 30

Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45

Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln 50 55 60

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 65 70 75 80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu 85 90 95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Cys 100 \$105\$

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 \$140\$

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser $165 \\ 170 \\ 175$

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

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Leu Met Tyr Thr Val Val Thr Pro 210 215

<210> 390

<211> 649

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	c to									ır Me					g cag u Gln	49
		_	_	_	gac Asp						_					97
caa Gln	aca Thr	tac Tyr 35	ttc Phe	ttt Phe	atg Met	gtt Val	ttt Phe 40	gga Gly	gat Asp	atg Met	gag Glu	agc Ser 45	ttc Phe	ctt Leu	ctt Leu	145
gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctg Leu	cat His	193
					agt Ser 70											241
ttg Leu	tgg Trp	atg Met	cta Leu	aca Thr 85	aca Thr	tcc Ser	cat His	gcc Ala	atg Met 90	atg Met	cat His	act Thr	ctc Leu	ctt Leu 95	gca Ala	289
gca Ala	aga Arg	ttg Leu	tct Ser 100	ttt Phe	tgt Cys	gag Glu	aac Asn	aat Asn 105	gtg Val	atc Ile	ctc Leu	aat Asn	ttt Phe 110	ttc Phe	tgt Cys	337
gac Asp	cta Leu	ttt Phe 115	gtt Val	ctc Leu	cta Leu	aag Lys	ctg Leu 120	gct Ala	tgc Cys	tca Ser	gac Asp	act Thr 125	tat Tyr	gtt Val	aat Asn	385
gag Glu	ttg Leu 130	atg Met	ata Ile	ttt Phe	ata Ile	atg Met 135	agt Ser	tcc Ser	ctc Leu	ctc Leu	att Ile 140	gtt Val	att Ile	cca Pro	ttt Phe	433
ttc Phe 145	ctc Leu	att Ile	gtc Val	atg Met	tct Ser 150	tat Tyr	gca Ala	agg Arg	atc Ile	att Ile 155	gcc Ala	tcc Ser	att Ile	ctt Leu	aag Lys 160	481
gtt Val	cca Pro	tct Ser	att Ile	caa Gln 165	Gly aaa	atc Ile	tac Tyr	aag Lys	gtc Val 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggt Gly 175	tcc Ser	529
cat His	ctg Leu	tct Ser	gtg Val 180	gtg Val	acc Thr	ttg Leu	ttt Phe	tat Tyr 185	Gly	aca Thr	att Ile	att Ile	ggt Gly 190	ctc Leu	tac Tyr	577
					aat Asn											625
_	_				gtg Val											649

- <210> 391
- <211> 216
- <212> PRT
- <213> Mus musculus domesticus
- <220>
- <221> misc_feature
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- <400> 391
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- Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
- Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
- Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
- Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu
- Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala
- Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys
- Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn
- Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe 135
- Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys 155 1.50
- Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser 165
- His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185
- Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala 200 205

<210> 392 <211> 649 <212> DNA <213> Mus musculus domesticus
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<220> <221> CDS <222> (2)(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7
<pre><400> 392 c ttt gca gac atc tgc ttt act tct gct agc atc cca aag atg cta gtg Phe Ala Asp Ile Cys Phe Thr Ser Ala Ser Ile Pro Lys Met Leu Val 1 5 10 15</pre>
aat ata cag aca aag aac aag gtg ata acc tat gaa ggt tgc att tct 97 Asn Ile Gln Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile Ser 20 25 30
caa gta ttc ttt ttc ata cta ttt gga gtt tta gat aac ttt ctt cta Gln Val Phe Phe Phe Ile Leu Phe Gly Val Leu Asp Asn Phe Leu Leu 35 40 45
gct gtg atg gcc tat gac cga tat gtg gca atc tgt cac cct ctg cac Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50 55 60
tat atg gtc atc atg aac cgc cgc ctc tgt gga ttt tta gtt ttg ggg Tyr Met Val Ile Met Asn Arg Arg Leu Cys Gly Phe Leu Val Leu Gly 70 75 80
tct tgg gtc aca aca gca ttg aat tcc ttg ctg cag agt tca atg gca 289 Ser Trp Val Thr Thr Ala Leu Asn Ser Leu Leu Gln Ser Ser Met Ala 85 90 95
ctg cgg ctg tcc ttt tgt aca gac ttg aaa att ccc cac ttt gtt tgt Leu Arg Leu Ser Phe Cys Thr Asp Leu Lys Ile Pro His Phe Val Cys 100 105 110
gag ctt aat caa ctg gta cta ctt gcc tgt aat gac acc ttt cct aat Glu Leu Asn Gln Leu Val Leu Leu Ala Cys Asn Asp Thr Phe Pro Asn 115 120 125
gac atg gtg atg tac ttt gca gct ata ctg ctg ggt ggt ggt cct ctt Asp Met Val Met Tyr Phe Ala Ala Ile Leu Leu Gly Gly Gly Pro Leu 130 135 140
gct ggc atc ctt tac tct tat tct aag ata gtt tcc tcc ata cgt gca Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 160
atc tca tca cag ggg aag tat aaa gca tcc tcc acc tgt gca tcc 529 Ile Ser Ser Ser Gln Gly Lys Tyr Lys Ala Ser Ser Thr Cys Ala Ser 165 170 175

Met Met Tyr Thr Val Val Thr Pro 210 215

cac ctc tca gtt gtt tca tta ttc tat tct aca ctc ttg ggt gcg His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala 180 185 190	
ctt agt tct tct ttt aca caa aac tca cac tca act gca cga gca Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala 195 200 205	
gtt atg tac agt gtg gtc acc ccc Val Met Tyr Ser Val Val Thr Pro 210 215	649
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<400> 393	
Phe Ala Asp Ile Cys Phe Thr Ser Ala Ser Ile Pro Lys Met Leu 1 5 10 15	Val
Asn Ile Gln Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile 20 25 30	Ser
Gln Val Phe Phe Phe Ile Leu Phe Gly Val Leu Asp Asn Phe Leu 35 40 45	Leu
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu 50 55 60	His
Tyr Met Val Ile Met Asn Arg Arg Leu Cys Gly Phe Leu Val Leu 65 70 75	Gly 80
Ser Trp Val Thr Thr Ala Leu Asn Ser Leu Leu Gln Ser Ser Met 85 90 95	Ala
Leu Arg Leu Ser Phe Cys Thr Asp Leu Lys Ile Pro His Phe Val	Сув
Glu Leu Asn Gln Leu Val Leu Leu Ala Cys Asn Asp Thr Phe Pro 115 120 125	Asn
Asp Met Val Met Tyr Phe Ala Ala Ile Leu Leu Gly Gly Pro 130 135 140	Leu
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg 145 150 155	Ala 160
Ile Ser Ser Ser Gln Gly Lys Tyr Lys Ala Ser Ser Thr Cys Ala	Ser

165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr
180 185 190

Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser 195 200 205

Val Met Tyr Ser Val Val Thr Pro 210 215

<210> 394

<211> 649

<212> DNA

<213> Mus musculus domesticus

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<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

aac atg cag agc cag gac tca tcc atc acc tat gca gga tgc ctg aca

Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr

20
25
30

caa atg tac ttt ttc ttg ctc ttt gga gac ctt gag agc ttc ctc ctt 145 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu

gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc ccc ctt cat

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His

50 60

tac atg agc atc atg agc ccc agc ctc tgt gtg agt ctg gtg ctg ctg

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu

65 70 75 80

tcc tgg gtg ctg acc act ttc cat gcc atg ctg cat acc ctg ctc atg

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met

85
90
95

gcc aga ttg tca ttc tgt gag gac aat gtg atc ccc tac ttt ttc tgt
Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro Tyr Phe Phe Cys

gac atg tct gct ctg ctg aag ctg tcc tgc tct gac act cac gtt aat 385
Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
115 120 125

gaa ttg gtg ata ttt gtc aca gga ggc ctg atc ctt gtc att cca ttt 433 Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe

130	135	140
gtg ctc atc ctt gtg to Val Leu Ile Leu Val Se 145	r Tyr Ala Arg Ile Va	
gtc ccg tct gct cga gg Val Pro Ser Ala Arg Gl 165		
cac ctg tct gtg gtg to His Leu Ser Val Val Se 180		ca atc att ggt ctg tac 577 nr Ile Ile Gly Leu Tyr 190
		ag gaa act gtc atg gcc 625 ys Glu Thr Val Met Ala 205
atg atg tac aca gtg gt Met Met Tyr Thr Val Va 210		649
<210> 395 <211> 216 <212> PRT <213> Mus musculus do	omesticus	
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<400> 395		
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Phe Ser Asp Leu Cys Pl 1 5	10	et Pro Lys Leu Leu Gln
Phe Ser Asp Leu Cys Pl 1 5 Asn Met Gln Ser Gln A 20	10 sp Ser Ser Ile Thr T 25	et Pro Lys Leu Leu Gln 15 yr Ala Gly Cys Leu Thr
Phe Ser Asp Leu Cys Plant Ser Gln A 20 Gln Met Tyr Phe Phe L 35	sp Ser Ser Ile Thr T 25 eu Leu Phe Gly Asp I 40	et Pro Lys Leu Leu Gln 15 yr Ala Gly Cys Leu Thr 30 eu Glu Ser Phe Leu Leu
Phe Ser Asp Leu Cys Photo Ser Asp Met Gln Ser Gln A 20 Gln Met Tyr Phe Phe L 35 Val Ala Met Ala Tyr A 50	sp Ser Ser Ile Thr T 25 eu Leu Phe Gly Asp L 40 sp Arg Tyr Val Ala I 55 er Pro Ser Leu Cys V	et Pro Lys Leu Leu Gln 15 yr Ala Gly Cys Leu Thr 30 eu Glu Ser Phe Leu Leu 45 le Cys Phe Pro Leu His
Phe Ser Asp Leu Cys Plant Ser Gln Agn Met Gln Ser Gln Agn Ser Gln Agn Ser Gln Agn Ser	sp Ser Ser Ile Thr T 25 eu Leu Phe Gly Asp L 40 sp Arg Tyr Val Ala I 55 er Pro Ser Leu Cys V	et Pro Lys Leu Leu Gln 15 yr Ala Gly Cys Leu Thr 30 eu Glu Ser Phe Leu Leu 45 le Cys Phe Pro Leu His 60 fal Ser Leu Val Leu Leu
Phe Ser Asp Leu Cys Plant Ser Gln Agn Met Gln Ser Gln Agn Fer Gln Agn Ser Gln Agn Ser Gln Agn Fer Fer Ser Trp Val Leu Thr Tass	sp Ser Ser Ile Thr T 25 eu Leu Phe Gly Asp L 40 sp Arg Tyr Val Ala I 55 er Pro Ser Leu Cys V 0 7	et Pro Lys Leu Leu Gln 15 yr Ala Gly Cys Leu Thr 30 eu Glu Ser Phe Leu Leu 45 le Cys Phe Pro Leu His 60 fal Ser Leu Val Leu Leu 80 eu His Thr Leu Leu Met

130 135 140
Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 145 150 155 160
Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190
Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala 195 200 205
Met Met Tyr Thr Val Val Thr Pro 210 215
<210> 396 <211> 649 <212> DNA <213> Mus musculus domesticus
<220> <221> misc_feature <222> (1)(649) <223> Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenBank = AF073972
<220> <221> CDS <222> (2)(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7
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c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln 1 5 10 15 aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
C ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln 1 5 10 15 aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30 caa atg tac tcc ttt ttg ttt ttc ggt gat gtt gag agt tta ctc ctt Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln 1 5 10 15 aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30 caa atg tac ttc ttt ttg ttt ttc ggt gat gtt gag agt tta ctc ctt Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu 35 40 gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc ttc cct ctt cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His

act agg ttg tct ttc tgt aaa aac aat gtg atc ccc cat ttt ttc t Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe C 100 105 110	tgt 337 Cys
gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att a Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile A 115 120 125	aat 385 Asn
gag tta atg ata atg ata att gga gca ctt gtt gtt ata ctt cca t Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro F 130 135 140	ttt 433 Phe
cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc att ctc a Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu I 145 150 155	aaa 481 Lys 160
gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggg t Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly S 165 170 175	tct 529 Ser
cat ctg tct gtg gtg tca ctg ttc tat ggg tca gtc att gtt ctg t His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu T 180 185 190	tac 577 Fyr
tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg t Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met S 195 200 205	act 625 Ser
atg atg tac act gtg gtg att ccc Met Met Tyr Thr Val Val Ile Pro 210 215	649
<210> 397 <211> 216 <212> PRT <213> Mus musculus domesticus	
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<pre><221> misc_feature <222> (1)(649) <223> Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenE <400> 397 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu G 1</pre>	Gln Ala
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<pre> <221> misc_feature <222> (1)(649) <223> Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenE <400> 397 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu G 1</pre>	Gln Ala Leu His

85

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Cys 105

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe 135

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 150 155

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 200

Met Met Tyr Thr Val Val Ile Pro

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<211> 649

<212> DNA <213> Mus musculus domesticus

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<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR27M; Accession DDBJ/EMBL/GenBank = AF073973

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<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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97 aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala

caa atg tac ttc ttt ttg ttt ttt ggt gat gtt gag agt tta ctc ctt 145 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu 40

gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc tcc cct ctt cat 193 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His

	50					55					60						
tat Tyr 65	acc Thr	aga Arg	atc Ile	atg Met	agc Ser 70	cca Pro	aac Asn	ctc Leu	tgt Cys	gtg Val 75	agt Ser	atg Met	gtg Val	ctg Leu	ctg Leu 80		241
tcc Ser	tgg Trp	gca Ala	ctg Leu	aca Thr 85	aca Thr	ttg Leu	tat Tyr	gcc Ala	atg Met 90	ttg Leu	cac His	act Thr	ttg Leu	ctc Leu 95	tta Leu		289
act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	aaa Lys	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys		337
gac Asp	ctt Leu	tct Ser 115	gct Ala	ctc Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn		385
		atg Met															433
		atc Ile															481
_		tca Ser		_				_	_				_				529
	_	tct Ser				_					_		_	_			577
	_	cca Pro 195									-		_	_			625
_	_	tac Tyr															649
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Phe 1	Thr	Asp	Leu	Cys 5	Phe	Ser	Thr	Val	Thr 10	Met	Pro	Asn	Phe	Leu 15	Gln		
Asn	Met	Gln	Ser 20	Gln	Val	Ser	Ser	Ile 25	Pro	Tyr	Ala	Gly	Cys 30	Leu	Ala		
Gln	Met	Tyr 35	Phe	Phe	Leu	Phe	Phe 40	Gly	Asp	Val	Glu	Ser 45	Leu	Leu	Leu		

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Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His
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Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
                    70
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Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 120

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Thr Leu Lys

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 180 185 190

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 195 200 205

Met Met Tyr Thr Val Val Thr Pro 210 215

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<213> Mus musculus domesticus

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<220>

<221> CDS

<222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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cac His	ttc Phe	ctc Leu	atg Met 20	gag Glu	aaa Lys	aag Lys	acc Thr	atc Ile 25	tct Ser	ttt Phe	gcc Ala	cta Leu	tgt Cys 30	Gly aaa	acc Thr	9	7
cag Gln	ctc Leu	ttc Phe 35	ttt Phe	gct Ala	ctg Leu	act Thr	ctt Leu 40	glà aaa	gga Gly	act Thr	gag Glu	ttt Phe 45	ctg Leu	ttg Leu	ctg Leu	14	5
act Thr	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gct Ala	gtc Val	tgt Cys 60	aat Asn	cca Pro	tta Leu	cgg Arg	19	3
		gtg Val														24	1
tct Ser	tgg Trp	ttt Phe	gtg Val	ggt Gly 85	gta Val	gtt Val	aat Asn	tct Ser	gct Ala 90	gtg Val	gag Glu	aca Thr	gca Ala	gtc Val 95	acc Thr	28	9
		ctt Leu														33	7
		ctg Leu 115														38	5
		gtg Val		_	_		_				_	_			_	43	3
		gtc Val														48	1
		tct Ser														52	9
	_	act Thr		_		_				_	_					57	7
		cct Pro 195														62	5
		tat Tyr														64	9
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Val Val Asp Ile Cys Tyr Thr Ser Ser Gly Val Pro Gln Met Leu Ala

His Phe Leu Met Glu Lys Lys Thr Ile Ser Phe Ala Leu Cys Gly Thr 20 25 30

Gln Leu Phe Phe Ala Leu Thr Leu Gly Gly Thr Glu Phe Leu Leu 35 40 45

Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg 50 55 60

Tyr Thr Val Val Met Asn Pro Arg Leu Cys Met Gly Leu Ala Gly Val 65 70 75 80

Ser Trp Phe Val Gly Val Val Asn Ser Ala Val Glu Thr Ala Val Thr 85 90 95

Glu Thr Leu Ala Leu Val Arg Leu Ala Cys Val Asp Ile Thr Leu Asn 115 120 125

Gln Val Val Ile Leu Ala Ser Ser Val Val Val Leu Met Ile Pro Cys 130 140

Ile Arg Ser Thr Gln Gly Arg Arg Lys Ala Phe Glu Thr Cys Ala Ser 165 170 175

His Leu Thr Val Val Ser Met Ser Tyr Gly Met Ala Leu Phe Thr Tyr 180 185 190

Leu Gln Pro Ala Ser Thr Ala Ser Ala Glu Gln Asp Lys Val Val Val 195 200 205

Ile Phe Tyr Ala Leu Val Thr Pro 210 215

<210> 402

<211> 649

<212> DNA

<213> Mus musculus domesticus

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<221> misc_feature

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					aag Lys											97
					gat Asp											145
	_	_			gat Asp	_		_	_		_			_		193
					tct Ser 70											241
					ttg Leu											289
					tgc Cys											337
_					ctg Leu	-			-							385
_				_	tcc Ser		_						~		-	433
					tcc Ser 150											481
					ggc Gly											529
					gct Ala											577
	_				gtc Val	_		-	_							625
					gtt Val											649
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<210> 403 <211> 216 <212> PRT

<213> Mus musculus domesticus <221> misc_feature <222> (1)..(649)
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Val Phe Tyr Thr Ile Val Val Pro 210 215

<210> 404

Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys Val Ser Ser

<211 <212 <213	?> I	649 DNA Mus n	nuscu	ılus	dome	estic	us									
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<220 <221 <222 <223 TM2	.> (acto	ory r	recep	otor;	reg	jion	betw	veen	tran	ısmen	mbrane	domains
	cac									ır Me					g cag eu Gln	49
		cag Gln														97
		tac Tyr 35														145
		atg Met														193
		agc Ser														241
		ttg Leu	_		_				_	_			_			289
act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	gaa Glu	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	337
		tct Ser 115														385
		gtg Val														433
cta Leu 145	ctc Leu	gtc Val	aca Thr	gtg Val	tct Ser 150	tat Tyr	gca Ala	cgc Arg	atc Ile	atc Ile 155	tcc Ser	tcc Ser	att Ile	ctc Leu	aag Lys 160	481
		tca Ser														529
		tct Ser														577
		cca Pro														625

ctg atg tac act gtg gta act ccc Leu Met Tyr Thr Val Val Thr Pro

649

<210> 405

<211> 216

<212> PRT

<213> Mus musculus domesticus

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<222> (1)..(649)
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<400> 405

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Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu 70

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 105

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 120

Glu Leu Val Ile Leu Ile Gly Gly Leu Val Val Ile Leu Pro Phe 130 135 140

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 145 150 155

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 195 200 205

Leu Met Tyr Thr Val Val Thr Pro 210 215

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cag aa Gln As															95	
aca ca Thr Gl															143	
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caa ta Gln Ty 65	r Ser														239	
ttc tg Phe Cy 80															287	
ttg go Leu Al	_	_			-	-								_	335	
tgt ga Cys As															383	
aat ga Asn Gl		Met													431	
ctc tt Leu Le						Tyr					Ser				479	

155

150

agg a Arg I 160																527	
tca c Ser H																575	
tac t Tyr I																623	
tcc c Ser I																650	
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Gln N	Met	Tyr 35	Phe	Phe	Ser	Val	Phe 40	Gly	Ser	Leu	Glu	Ile 45	Phe	Leu	Leu		
Val V	Val 50	Leu	Ala	Tyr	Asp	Arg 55	Tyr	Val	Ala	Ile	Cys 60	Leu	Pro	Leu	Gln		
Tyr 8	Ser	Ser	Ile	Met	Ser 70	Pro	Asn	Leu	Cys	Val 75	Cys	Val	Val	Val	Phe 80		
Cys 5	Trp	Val	Phe	Ile 85	Val	Phe	Tyr	Ala	Met 90	Phe	His	Thr	Leu	Leu 95	Leu		
Ala A	Arg	Leu	Ser 100	Phe	Cys	Lys	Asn	Asn 105		Ile	Pro	His	Phe 110	Phe	Cys		
Asp :	Ile	Ser 115	Ala	Leu	Leu	Lys	Leu 120	Ala	Cys	Ser	Asp	Val 125	Tyr	Ile	Asn		
Glu 1	Leu 130	Met	Ile	Leu	Ile	Leu 135	_	Gly	Phe	Leu	Leu 140		Thr	Ser	Leu		
Leu :	Leu	Ile	Ile	Val	Ser	Tyr	Val	Gln	. Ile		Ser	Ser	Ile	Leu	Arg		

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 200

Leu Met Tyr Thr Val Val Thr Pro 210 215

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<221> CDS

<222> (2)..(646)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg aca 97 Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr

caa atg tac ttt ttc agt gtt ttt ggg agt ctg gag ata ttc ctt ctt 145 Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 40

gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt caa 193 Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln

tat tee age ate atg age eee aat ete tgt gtg tgt gtg gtg gtg tte 241 Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 70 75 65

tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc ttg 289 Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu

gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc tgt 337 Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 105

gac ata tot goo oft otg aag ttg goa tgc tot gat gtt tat att aat 385 Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn

		115					120					125				
	tta Leu 130															433
	ctc Leu			_			_			_						481
	tct Ser															529
	ctg Leu															577
	tgt Cys															625
_	atg Met 210						CC									648
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Gln	. Met	Tyr 35	Phe	Phe	Ser	Val	Phe 40	Gly	Ser	Leu	Glu	Ile 45	Phe	Leu	Leu	
Val	Val 50	Leu	Ala	Tyr	Asp	Arg 55	Tyr	Val	Ala	Ile	Cys 60	Leu	Pro	Leu	Gln	
Туг 65	Ser	Ser	Ile	Met	Ser 70	Pro	Asn	Leu	Cys	Val 75	Cys	Val	Val	Val	Phe 80	
Cys	Trp	Val	Phe	Ile 85	Val	Phe	Tyr	Ala	Met 90	Phe	His	Thr	Leu	Leu 95	Leu	

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125
Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135 140
Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160
Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190
Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205
Leu Met Tyr Thr Val Val Thr 210 215
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aac atg cag agc cag gac cca tcc atc ccc tat gcc agc tgt ctg aca Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Ser Cys Leu Thr 20 25 30
caa atg tac ttt ttc atg gct ttt ggg aac atg gaa att tat ctt ctt Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu 35 40 45
gtg gtc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctt cat Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60
tac acc agc atc atg agc cct aag ctc tgt gtg tct ctg gtg gtt ctc Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu 70 75 80

tct tgg gta ttt acc att ctg tat tcc atg tta cac acc cta ctc ttg Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu Leu 85 90 95	289
gca aga ttg tca ttc tgt gag gac aat gtg atc ccc cac ttt ttc tgt Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys 100 105 110	337
gac ata tot god otg otd aag ttg god tgd tot gad att tot att aat Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Ser Ile Asn 115 120 125	385
gaa cta atg ata ttt atc gtg gga ggg ctt gat act gta atc cca ttt Glu Leu Met Ile Phe Ile Val Gly Gly Leu Asp Thr Val Ile Pro Phe 130 135 140	433
tta ctc att gtt tcc tat gta caa att gtc tgc tcc att cta aag Leu Leu Ile Val Val Ser Tyr Val Gln Ile Val Cys Ser Ile Leu Lys 145 150 155 160	481
ttc tca tct aca cgg ggc ata cac aag gtc ttc tcc acc tgt ggc tcc Phe Ser Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	529
cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt gtc tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr 180 185 190	577
ata tgc cca tca gct aat aac tct act gtg aag gag act gtc atg tcc Ile Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser 195 200 205	625
ctg atg tac aca gtg gtg acg ccc Leu Met Tyr Thr Val Val Thr Pro 210 215	649
<210> 411 <211> 216 <212> PRT <213> Mus musculus domesticus	
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Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu 35 40 45	
Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60	
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu	

Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu Leu

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys 105

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Ser Ile Asn 120 125

Glu Leu Met Ile Phe Ile Val Gly Gly Leu Asp Thr Val Ile Pro Phe 130 135 140

Leu Leu Ile Val Val Ser Tyr Val Gln Ile Val Cys Ser Ile Leu Lys

Phe Ser Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr 185

Ile Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser 200

Leu Met Tyr Thr Val Val Thr Pro 210

<210> 412

<211> 649

<212> DNA <213> Mus musculus domesticus

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<220>

<221> CDS

<222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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97 aac atg cag age caa gtt eet tea ate eee tat gea gge tge etg aca Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr

caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu 145

		35					40					45						
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tac Tyr 65	acc Thr	agc Ser	att Ile	atg Met	agc Ser 70	ccc Pro	agg Arg	ctc Leu	tgt Cys	gtg Val 75	agt Ser	ctt Leu	gtg Val	ctg Leu	ctg Leu 80		24	1
		ttg Leu															28	39
		ttg Leu															33	37
		tct Ser 115		_	_	_	_	_	-		_						38	35
-	_	gtg Val	_	_						_	_						43	3
		gtc Val						_							_		48	31
_		tca Ser		_				_	_				_				52	29
		tct Ser															57	77
	~	cca Pro 195		~						_	-		_	_			62	25
_	_	tac Tyr			_												64	19
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Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 20 25 30

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Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
                            40
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Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
                        55
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Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 105

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe

Leu Leu Val Thr Val Pro Tyr Ala Arq Ile Ile Ser Ser Ile Leu Lys 150

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 195

Leu Met Tyr Thr Val Val Thr Pro

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<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30	97
caa atg tac ttc ttt ttg ttt ttt ggt gat gtt gag agc tta ctc ctt Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu 35 40 45	145
gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc ttc cct ctt cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60	193
tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu 65 70 75 80	241
tcc tgg gca ctg aca aca ttg tat gcc atg ttg cac act ttg ctc tta Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu 85 90 95	289
act agg ttg tct ttc tgt aaa aac aat gtg atc ccc cat ttt ttc tgt Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110	337
gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att aat Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125	385
gag tta atg ata atg ata att gga gca ctt gtt gtt ata ctt cca ttt Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe 130 135 140	433
cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc att ctc aaa Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 145 150 155 160	481
gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	529
cat ctg tct gcg gtg tca ctg ttc tat ggg tca gtc att gtt ctg tac His Leu Ser Ala Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 180 185 190	577
tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg tct Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 195 200 205	625
atg atg tac act gtg gtg act ccc Met Met Tyr Thr Val Val Thr Pro 210 215	649
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Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55

Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 105

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe 135

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170

His Leu Ser Ala Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 185

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 195 200

Met Met Tyr Thr Val Val Thr Pro 210

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aat Asn	ata Ile	cag Gln	agc Ser 20	cag Gln	gac Asp	cca Pro	tcc Ser	atc Ile 25	ccc Pro	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	ctg Leu	gca Ala		97
caa Gln	aca Thr	tac Tyr 35	ttc Phe	ttt Phe	atg Met	gtt Val	ttt Phe 40	gga Gly	gat Asp	atg Met	gag Glu	agc Ser 45	ttc Phe	ctt Leu	ctt Leu	1	45
gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctg Leu	cat His	1	93
tac Tyr 65	acc Thr	agc Ser	atc Ile	atg Met	agt Ser 70	ccc Pro	aaa Lys	ctc Leu	tgt Cys	ggt Gly 75	tgt Cys	cta Leu	atg Met	ctg Leu	cta Leu 80	2	41
ttg Leu	tgg Trp	atg Met	cta Leu	aca Thr 85	aca Thr	tcc Ser	cat His	gcc Ala	atg Met 90	atg Met	cat His	act Thr	ctc Leu	ctt Leu 95	gca Ala	2	89
gca Ala	aga Arg	ttg Leu	tct Ser 100	ttt Phe	tgt Cys	gag Glu	aac Asn	aat Asn 105	gtg Val	atc Ile	ctc Leu	aat Asn	ttt Phe 110	ttc Phe	tgt Cys	3	37
gac Asp	cta Leu	ttt Phe 115	gta Val	ctc Leu	cta Leu	aag Lys	ctg Leu 120	gct Ala	tgc Cys	tca Ser	gac Asp	act Thr 125	tat Tyr	gtt Val	aat Asn	3	85
gag Glu	ttg Leu 130	atg Met	ata Ile	ttt Phe	ata Ile	atg Met 135	agt Ser	tcc Ser	ctc Leu	ctc Leu	att Ile 140	gtt Val	att Ile	cca Pro	ttt Phe	4	33
ttc Phe 145	ctc Leu	att Ile	gtc Val	atg Met	tct Ser 150	tat Tyr	gca Ala	agg Arg	atc Ile	att Ile 155	gcc Ala	tcc Ser	att Ile	ctt Leu	aag Lys 160	4	81
gtt Val	cca Pro	tct Ser	att Ile	caa Gln 165	gly ggg	atc Ile	tac Tyr	aag Lys	gtc Val 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggt Gly 175	tcc Ser	5	29
cat His	ctg Leu	tct Ser	gtg Val 180	gtg Val	acc Thr	ttg Leu	ttt Phe	tat Tyr 185	gly aaa	aca Thr	att Ile	att Ile	ggt Gly 190	ctc Leu	tac Tyr	5	77
tta Leu	tgt Cys	cca Pro 195	tca Ser	ggt Gly	aat Asn	aat Asn	tcc Ser 200	aca Thr	gta Val	aag Lys	gly aaa	act Thr 205	gtc Val	atg Met	gcc Ala	6	25
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Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
                        55
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu
                    70
Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala
                85
                                    90
Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys
            100
Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn
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Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala 195 200 205

Met Met Tyr Thr Ala Val Thr Pro

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TM2 and TM7
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aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc
Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
            20
cag atg tct gtc ttc ttg gtt ttt gca gaa ttg gac aac ttt ctc ctg
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Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu
gct gtg atg gcc tat gac cga tat gtg gct atc tgt cac cca tta tat
                                                                      193
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
tac aca gtc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg
                                                                      241
Tyr Thr Val Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu
                    70
tcc tgg gtt gtt agc atc cta cat gcc ttc tta cag agc tca att gtg
                                                                      289
Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val
                85
                                    90
cta cag ttg acc ttt tgt gga gat gta aaa att ccc cac ttc ttc tgt
                                                                      337
Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys
            100
                                105
                                                    110
gag ctt aac cag ctg tct caa ctc aca tgt tca gac agc ttt tca agc
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Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Phe Ser Ser
                            120
caa ctc ata atg aat ctt gta cct gtt cta ttg gca gtc att tcc ttc
                                                                      433
Gln Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe
                        135
agt agt atc ctt tac tct tat ttc aag ata gtg tcc tcc ata tgt tct
                                                                      481
Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser
atc tcc tca gtt caa ggg aag tac aag gca ttt tct aca tgt gtc tct
                                                                      529
Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
                165
cac ctt tcc att gtc tcc tta ttt tat agt aca ggc ctt gga gtg tat
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His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr 180 185 gtc agt tct gtg atc caa agc tct cac tct gct gca aga gcc tct 625 Val Ser Ser Val Val Ile Gln Ser Ser His Ser Ala Ala Arg Ala Ser 200 205 gtg atg tat act gtg gtc acc ccg 649 Val Met Tyr Thr Val Val Thr Pro <210> 419 <211> 216 <212> PRT <213> Mus musculus domesticus <220> <221> misc_feature <222> (1). (649)
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Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser

His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr 185

Val Ser Ser Val Val Ile Gln Ser Ser His Ser Ala Ala Arg Ala Ser

Val Met Tyr Thr Val Val Thr Pro

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<211> 646

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cag ctg tat ttt ctc tgt gtg ttt gct gac atg gac aat ttc ctg ctg 145 Gln Leu Tyr Phe Leu Cys Val Phe Ala Asp Met Asp Asn Phe Leu Leu 35

gct gtg atg gcc tat gac cga ttt gtg gcc ata tgc cac cct tta cac 193 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50

tac aca aca aag atg acc cat cag ctt tgt gcc ttt ctt gtt gtt ggg 241 Tyr Thr Thr Lys Met Thr His Gln Leu Cys Ala Phe Leu Val Val Gly

tee tgg atg gta gee agt etg aat get etg ttg cae aca etg ete gtg 289 Ser Trp Met Val Ala Ser Leu Asn Ala Leu Leu His Thr Leu Leu Val 90

gct caa ctc tac ttc tgt ggg gac aat gtg atc ccc cac ttc ttc tgt 337 Ala Gln Leu Tyr Phe Cys Gly Asp Asn Val Ile Pro His Phe Phe Cys 105

gaa gtg act ccc ctg ctg aaa ctc tct tgc tca gac aca cat ctc aat 385 Glu Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn 115 120

gag ttg atg att ctt gct gtt gca ggg ctg ata atg tta gct cca ttt 433

Glu	Leu 130	Met	Ile	Leu	Ala	Val 135	Ala	Gly	Leu	Ile	Met 140	Leu	Ala	Pro	Phe	
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atc Ile	tca Ser	tcc Ser	aca Thr	gga Gly 165	aga Arg	tgg Trp	aaa Lys	gcc Ala	ttc Phe 170	tct Ser	acc Thr	tgt Cys	ggc Gly	tca Ser 175	cac His	529
ttg Leu	gct Ala	gtt Val	gtg Val 180	tgc Cys	ctc Leu	ttc Phe	tat Tyr	ggc Gly 185	act Thr	atc Ile	ata Ile	tcc Ser	ctg Leu 190	tat Tyr	ttc Phe	577
aac Asn	ccc Pro	tca Ser 195	tct Ser	tct Ser	cac His	tca Ser	gct Ala 200	gly ggg	agg Arg	gac Asp	atg Met	gca Ala 205	gct Ala	gcc Ala	atg Met	625
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115 120 125

Glu	Leu 130	Met	Ile	Leu	Ala	Val 135	Ala	Gly	Leu	Ile	Met 140	Leu	Ala	Pro	Phe	
Val 145	Cys	Ile	Leu	Leu	Ser 150	Tyr	Ile	Leu	Ile	Ala 155	Cys	Ala	Ile	Leu	Lys 160	
Ile	Ser	Ser	Thr	Gly 165	Arg	Trp	Lys	Ala	Phe 170	Ser	Thr	Cys	Gly	Ser 175	His	
Leu	Ala	Val	Val 180	Cys	Leu	Phe	Tyr	Gly 185	Thr	Ile	Ile	Ser	Leu 190	Tyr	Phe	
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cag Gln	atg Met	tct Ser 35	gtc Val	ttc Phe	ttg Leu	gtt Val	ttt Phe 40	gga Gly	gaa Glu	ctg Leu	gac Asp	aac Asn 45	ttt Phe	ctc Leu	ctg Leu	145
gct Ala	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	tat Tyr	gtg Val	gct Ala	atc Ile	tgt Cys 60	cac His	cca Pro	ttg Leu	tat Tyr	193
tac Tyr 65	aca Thr	ttc Phe	att Ile	gtt Val	aac Asn 70	caa Gln	cat His	ctc Leu	tgt Cys	ata Ile 75	ctg Leu	atg Met	gtt Val	ctg Leu	ctg Leu 80	241

tcc tgg gtt gtt agc atc cta cat gcc ttc tta cag agc tca att gta

Ser	Trp	Val	Val	Ser 85	Ile	Leu	His	Ala	Phe 90	Leu	Gln	Ser	Ser	Ile 95	Val	
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gag Glu	ctt Leu	aac Asn 115	cag Gln	ctg Leu	tct Ser	caa Gln	ctc Leu 120	aca Thr	tgt Cys	tca Ser	gac Asp	agc Ser 125	tta Leu	tca Ser	agc Ser	385
cac His	ctc Leu 130	ata Ile	atg Met	cat His	ctt Leu	gta Val 135	cct Pro	gtt Val	cta Leu	ttg Leu	gga Gly 140	gcc Ala	att Ile	tcc Ser	ttc Phe	433
agt Ser 145	agt Ser	atc Ile	ctt Leu	tac Tyr	tct Ser 150	tat Tyr	ttc Phe	aag Lys	ata Ile	gtg Val 155	tcc Ser	tcc Ser	ata Ile	tgt Cys	tct Ser 160	481
atc Ile	tcc Ser	tca Ser	gtt Val	caa Gln 165	Gly 999	aag Lys	tac Tyr	aag Lys	gca Ala 170	ttt Phe	tct Ser	aca Thr	tgt Cys	gtc Val 175	tct Ser	529
cac His	ctt Leu	tcc Ser	att Ile 180	gta Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	agt Ser	aca Thr	ggc Gly	ctt Leu	gga Gly 190	gtg Val	tat Tyr	577
gtc Val	agt Ser	tct Ser 195	gct Ala	gtg Val	gtc Val	caa Gln	agc Ser 200	tct Ser	cac His	tct Ser	gct Ala	gca Ala 205	aga Arg	gcc Ala	tct Ser	625
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Gln	Met	Ser 35	Val	Phe	Leu	Val	Phe 40	Gly	Glu	Leu	Asp	Asn 45	Phe	Leu	Leu	
Ala	Val 50	Met	Ala	Tyr	Asp	Arg 55	Tyr	Val	Ala	Ile	Cys 60	His	Pro	Leu	Tyr	
Tyr	Thr	Phe	Ile	Val	Asn	Gln	His	Leu	Cys	Ile	Leu	Met	Val	Leu	Leu	

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val

Leu Gln Leu Thr Phe Cys Gly Asp Val Arg Ile Pro His Phe Phe Cys

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Leu Ser Ser

His Leu Ile Met His Leu Val Pro Val Leu Leu Gly Ala Ile Ser Phe

Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser

His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr

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cag atg tot gto tto ttg gtt ttt gca gaa ttg gac aac ttt otc otg

Gln	Met	Ser 35	Val	Phe	Leu	Val	Phe 40	Ala	Glu	Leu	qaA	Asn 45	Phe	Leu	Leu		
					gac Asp												193
					aac Asn 70												241
					atc Ile												289
					tgt Cys												337
gag Glu	ctt Leu	aac Asn 115	cag Gln	ctg Leu	tct Ser	caa Gln	ctc Leu 120	aca Thr	tgt Cys	tta Leu	gac Asp	agc Ser 125	ttt Phe	tca Ser	agc Ser		385
					ctt Leu												433
agt Ser 145	agt Ser	atc Ile	ctt Leu	tac Tyr	tct Ser 150	tat Tyr	ttc Phe	aag Lys	ata Ile	gtg Val 155	tcc Ser	tcc Ser	ata Ile	tgt Cys	tct Ser 160		481
					gly aaa												529
cac His	ctt Leu	tcc Ser	att Ile 180	gtc Val	ttc Phe	tta Leu	ttt Phe	tat Tyr 185	agt Ser	aca Thr	ggc	ctt Leu	gga Gly 190	gtg Val	tat Tyr		577
gtc Val	agt Ser	tct Ser 195	gct Ala	gtg Val	gtc Val	caa Gln	agc Ser 200	tct Ser	cac His	tct Ser	gct Ala	gca Ala 205	aga Arg	gcc Ala	tct Ser		625
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Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr

Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val 90

Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Leu Asp Ser Phe Ser Ser

His Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe

Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser

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cac His	ttc Phe	ctg Leu	gtg Val 20	aag Lys	agg Arg	aag Lys	acc Thr	att Ile 25	tct Ser	ttt Phe	gct Ala	gga Gly	tgt Cys 30	tct Ser	aca Thr	97
cag Gln	ata Ile	gtg Val 35	gtg Val	ttg Leu	ctt Leu	ctg Leu	gtc Val 40	gga Gly	tgc Cys	aca Thr	gag Glu	tgt Cys 45	gca Ala	ctg Leu	ctg Leu	145
gca Ala	gtg Val 50	atg Met	tcc Ser	tat Tyr	gac Asp	cga Arg 55	tat Tyr	gtg Val	gct Ala	gtc Val	tgc Cys 60	aaa Lys	cct Pro	ctg Leu	cac His	193
tac Tyr 65	tcc Ser	acc Thr	atc Ile	atg Met	aca Thr 70	cac His	tgg Trp	cta Leu	tgt Cys	gtt Val 75	cag Gln	ctg Leu	gct Ala	gca Ala	80 GJA āāā	241
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tta Leu	cgt Arg	ctt Leu	cct Pro 100	tat Tyr	cga Arg	gga Gly	aac Asn	aat Asn 105	gtc Val	att Ile	aac Asn	cac His	ttt Phe 110	ttc Phe	tgt Cys	337
gaa Glu	cct Pro	cct Pro 115	gcc Ala	ctc Leu	ctg Leu	aag Lys	ctg Leu 120	gca Ala	tcg Ser	gca Ala	gat Asp	aca Thr 125	Tyr	agc Ser	aca Thr	385
gag Glu	atg Met 130	Ala	atc Ile	ttt Phe	gca Ala	atg Met 135	ggt Gly	gtg Val	gta Val	atc Ile	ctc Leu 140	. Leu	gca Ala	cct Pro	gtc Val	433
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atg Met	cag Glr	g tct n Ser	ggg Gly	gaa Glu 165	ιGly	agg Arg	ctc Leu	aag Lys	gto Val	. Pne	tcc Ser	acc Thi	tgt Cys	ggc Gly 175	tcc Ser	529
cac His	cto Lei	att ı Ile	gtt Val	. Val	gtt Val	cto Leu	tto Phe	tac Tyr 185	GL?	tca Sei	a gca Ala	a ata a Ile	ttte Phe	S Alc	tac Tyr	577
atg Met	agg Arg	g cco g Pro 199) Ası	c tct n Sei	aag Lys	g ata s Ile	atg Met 200	: Asr	gaa Glu	a aaq ı Lys	g gat s Asp	t aaa p Lys 20!	s Me	g att	tcg Ser	625
gtg Val	tto Pho 21	c tat e Ty:	t tca	a gca r Ala	a gto a Val	g aco l Thi 215	r	9								649
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Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys Pro Leu His 50 60

Tyr Ser Thr Ile Met Thr His Trp Leu Cys Val Gln Leu Ala Ala Gly 65 70 75 80

Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr Thr Phe Thr 85 90 95

Leu Arg Leu Pro Tyr Arg Gly Asn Asn Val Ile Asn His Phe Cys 100 105

Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ala Asp Thr Tyr Ser Thr 115 120 125

Glu Met Ala Ile Phe Ala Met Gly Val Val Ile Leu Leu Ala Pro Val 130 135 140

Ser Leu Ile Leu Thr Ser Tyr Trp Asn Ile Ile Ser Thr Val Ile Gln 145 150 155 160

Met Gln Ser Gly Glu Gly Arg Leu Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ile Val Val Leu Phe Tyr Gly Ser Ala Ile Phe Ala Tyr 180 185 190

Met Arg Pro Asn Ser Lys Ile Met Asn Glu Lys Asp Lys Met Ile Ser 195 200 205

Val Phe Tyr Ser Ala Val Thr Pro 210 215

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caa Gln	atg Met	tac Tyr 35	ttc Phe	ttt Phe	ttg Leu	ttt Phe	ttt Phe 40	gga Gly	gat Asp	ctt Leu	gag Glu	agc Ser 45	ttc Phe	ctc Leu	ctt Leu	145
gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	tat Tyr	gta Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctt Leu	cat His	193
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act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	gaa Glu	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	337
gat Asp	ctg Leu	tct Ser 115	gct Ala	ctg Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	385
gaa Glu	ttg Leu 130	gtg Val	ata Ile	ttg Leu	atc Ile	ata Ile 135	gga Gly	Gly aaa	ctt Leu	gtt Val	gtt Val 140	ata Ile	ctt Leu	cca Pro	ttt Phe	433
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cac His	ctg Leu	tct Ser	gtg Val 180	gtg Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly 999	aca Thr	att Ile	att Ile	ggc Gly 190	ctc Leu	tac Tyr	577
tta Leu	tgt Cys	cca Pro 195	Ser	gct Ala	aat Asn	aac Asn	tct Ser 200	act Thr	cta Leu	aag Lys	gac Asp	act Thr 205	Val	atg Met	tct Ser	625

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Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
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Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
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Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
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Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
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His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr

185

180

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90

cct aag atg ttg gtg aat atc caa aca cag agc aag tcc atc tcc tat Pro Lys Met Leu Val Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr

25

828

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													gtg Val			924
_							_						cta Leu 140	_		972
													tct Ser			1020
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Leu	Met	Phe 35	Val	Val	Ala	Val	Leu 40	Gly	Asn	Leu	Leu	Ile 45	Ile	Leu	Ala		
Val	Ser 50	Ile	Asp	Ser	His	Leu 55	His	Thr	Pro	Met	Tyr 60	Phe	Phe	Leu	Ser		
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Pro	Leu 130	His	Tyr	Ser	Val	Ile 135	Met	Asn	Pro	Gln	Leu 140	Ser	Gly	Leu	Leu		
Val 145	Leu	Val	Ser	Trp	Phe 150	Ile	Ser	Phe	Ser	Tyr 155	Ser	Leu	Ile	Gln	Ser 160		
Leu	Leu	Met	Leu	Arg 165	Leu	Ser	Phe	Cys	Thr 170	Asn	Gln	Ile	Ile	Lys 175	His		
Phe	Tyr	Cys	Glu 180	Tyr	Ala	Lys	Ala	Leu 185	Thr	Ile	Ala	Cys	Ser 190	Asp	Thr		

Leu Ile Asn His Ile Leu Leu Tyr Ile Val Ile Trp Val Leu Gly Phe \$195\$

Ile Pro Phe Ser Gly Ile Leu Tyr Ser Tyr Tyr Lys Ile Phe Ser Ser 210 215 220

Ile Leu Arg Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr 225 230225235

Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe 275 280 285

Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Lys Ala Leu Lys Thr Leu 290 295 300

Gly Arg Ile Leu Leu Leu Lys 305 310